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OM protein - protein search, using sw model

Run on: March 2, 2006, 19:29:36 ; Search time 142.364 Seconds
(without alignments)
1413.528 Million cell updates/sec

Title: US-10-618-320A-1
Perfect score: 2400
Sequence: 1 MGICYSLRPLLFQGGDDPC.....VFNDCRDIQRMHLKQYELL 458

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_21.*
1: Geneseqp1980s.*
2: Geneseqp1990s.*
3: Geneseqp2000s.*
4: Geneseqp2001s.*
5: Geneseqp2002s.*
6: Geneseqp2003as.*
7: Geneseqp2003bs.*
8: Geneseqp2004s.*
9: Geneseqp2005s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2400	100.0	458	8	ADG74722 Human G-p
2	2400	100.0	458	9	AEAI7292 Human XLG
3	2124	88.5	448	8	ADG74746 Mouse G-p
4	2113	88.0	450	8	ADG74747 Rat G-pro
5	1819	75.8	381	5	ABBO9272 G protein
6	1819	75.8	381	7	ADCO9607 Human G-p
7	1819	75.8	381	7	ADCO9607 Human Pro
8	1819	75.8	381	8	ADU60726 Human G-p
9	1819	75.8	381	9	ADX26261 Novel cel
10	1819	75.8	381	9	AEAI7294 Human Gol
11	1811	75.5	381	7	ADEG1905 Rat Prote
12	1559	65.0	756	5	ABG60299 Lymphona
13	1559	65.0	756	6	ABP97657 Amino aci
14	1559	65.0	909	8	ADQ26060 Guanine n
15	1559	65.0	909	8	ABM82265 Tumour-as
16	1559	65.0	909	9	ADX06936 Cyclin-de
17	1540	64.2	379	4	AAB99060 Human G-p
18	1540	64.2	379	5	ABBO9269 G protein
19	1540	64.2	379	7	ADCO9604 Human G-p
20	1540	64.2	379	7	ADJ68299 Human hea
21	1540	64.2	379	8	ADU60723 Human G-p
22	1537	64.0	720	6	ABP56694 GCR1:Gs f
23	1536.5	64.0	755	8	ADM79379 Mouse lym
24	1529.5	63.7	380	3	AAB23382 Human G-a

25	1529.5	63.7	380	4	AAB99058 Human G-p
26	1529.5	63.7	380	4	AAB99061 Human G-p
27	1529.5	63.7	380	5	ABB09270 G protein
28	1529.5	63.7	380	7	ADC09605 Human G-p
29	1529.5	63.7	380	7	ADP70778 Minicell
30	1529.5	63.7	380	8	ADQ26061 Guanine n
31	1529.5	63.7	380	8	ABM82267 Tumour-as
32	1529.5	63.7	380	8	ADU60724 Human G-p
33	1526.5	63.6	926	4	AAU04387 GPCR-Gs f
34	1526.5	63.6	926	7	ADL96550 G protein
35	1526.5	63.6	926	9	ADM44723 Human RUP
36	1526.5	63.6	926	9	AEB20907 Human RUP
37	1525.5	63.6	394	2	AAR94559 Human Gs
38	1525.5	63.6	394	5	ABB09267 G protein
39	1525.5	63.6	394	5	ABG60304 Lymphona
40	1525.5	63.6	394	6	ABP97662 Amino aci
41	1525.5	63.6	394	7	ABR82636 C. elegan
42	1525.5	63.6	394	7	ADC09602 Human G-p
43	1525.5	63.6	394	7	ADP70779 Minicell
44	1525.5	63.6	394	8	ADQ26059 Guanine n
45	1525.5	63.6	394	8	ABM82266 Tumour-as

ALIGNMENTS

RESULT 1
ADG74722
ID ADG74722 standard; protein; 458 AA.
XX
AC ADG74722;
XX
DT 22-APR-2004 (first entry)
XX
DE Human G-protein Gml amino acid sequence.
XX
KW G protein; Gml; G protein-coupled receptor mediated signal transduction;
KW GTP binding site; GTPase site; G protein alpha subunit;
KW signal transduction; G-protein-coupled receptor.
XX
OS Homo sapiens.
XX
FN EP1382613-A1.
XX
PD 21-JAN-2004.
XX
PF 09-JUL-2003; 2003EP-00015519.
XX
PR 16-JUL-2002; 2002JP-00206841.
PR 19-DEC-2002; 2002JP-00367778.
PR 31-MAR-2003; 2003JP-00095955.
XX
PA (SUMO) SUMITOMO CHEM CO LTD.
XX
PI Takahashi Y, Matsumoto Y, Oeda K;
DR WPI: 2004-111483/12.
DR N-PSDB; ADG74723.
XX
PT New protein useful as a therapeutic or prophylactic agent against a
PT disease caused by an abnormality in a G-protein coupled receptor mediated
PT signal transduction.
XX
PS Claim 1; SEQ ID NO 1; 85pp; English.
XX
CC This invention relates to a novel G protein (Gml). The protein is
CC involved in a G protein-coupled receptor mediated signal transduction.
CC The protein of the invention has a sequence with a high homology with a
CC GTP binding site and a GTPase site conserved among G protein alpha
CC subunits. The protein, the DNA sequence which encodes it and an antibody
CC specifically recognising the protein of the invention may be useful as a
CC therapeutic or prophylactic agent against a disease caused by an
CC abnormality in a G-protein coupled receptor mediated signal transduction.

CC The invention may also be useful for screening for a substance capable of
 CC regulating a signal transduction mediated by a G-protein-coupled receptor
 CC and a protein.

XX SQ Sequence 458 AA;

Query Match 100.0%; Score 2400; DB 8; Length 458;
 Best Local Similarity 100.0%; Pred. No. 6.3e-200;
 Matches 458; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGLCYSLRPLFLFGPGDDPCAASEPPVEDAQAPALAPVRAAARDTARTLLPRGEGS 60
 DB 1 MGLCYSLRPLFLFGPGDDPCAASEPPVEDAQAPALAPVRAAARDTARTLLPRGEGS 60

QY 61 PACARPKADPKPEKQRTQTEQLSAEREAAKEREAVKEARKVSGIDRMRLDQKRDLDQTH 120
 DB 61 PACARPKADPKPEKQRTQTEQLSAEREAAKEREAVKEARKVSGIDRMRLDQKRDLDQTH 120

QY 121 RLLLLGAGESGKSTIVKQMRILHVNGFNPEEKQKILDIRKNVKDAIVTVSAMSTIIPP 180
 DB 121 RLLLLGAGESGKSTIVKQMRILHVNGFNPEEKQKILDIRKNVKDAIVTVSAMSTIIPP 180

QY 181 VPLANPENQFRSDYIKSIAPITDFEYSQEFDFHVKKLWDDGVKACFERSNEYQLIDCAQ 240
 DB 181 VPLANPENQFRSDYIKSIAPITDFEYSQEFDFHVKKLWDDGVKACFERSNEYQLIDCAQ 240

QY 241 YFLERIDSVSLVDYPTDQDQLLCRVLTSGIFETRFQVDKVNFMFVGVGQDERRKWIQ 300
 DB 241 YFLERIDSVSLVDYPTDQDQLLCRVLTSGIFETRFQVDKVNFMFVGVGQDERRKWIQ 300

QY 301 CFNDVTAIYVAACSSYNMVIREDNNTNRLRESLDLFESINNNRWLRTISIIILFNKQDM 360
 DB 301 CFNDVTAIYVAACSSYNMVIREDNNTNRLRESLDLFESINNNRWLRTISIIILFNKQDM 360

QY 361 LAEKVLGSKIEDYFPEYANYTVPEDATPDAGEDPKVTRAKFFIRDLFLRISTATGDGK 420
 DB 361 LAEKVLGSKIEDYFPEYANYTVPEDATPDAGEDPKVTRAKFFIRDLFLRISTATGDGK 420

QY 421 HCYCPHFTCAVDTENIRRVFNDCRDIIQRMHLKQYELL 458
 DB 421 HCYCPHFTCAVDTENIRRVFNDCRDIIQRMHLKQYELL 458

RESULT 2

AEAL17292 standard; protein; 458 AA.

XX AC AEAL17292;

XX AC AEAL17292;

XX AC AEAL17292;

XX AC AEAL17292;

XX AC AEAL17292;

XX AC AEAL17292;

XX AC AEAL17292;

XX AC AEAL17292;

XX AC AEAL17292;

XX AC AEAL17292;

XX AC AEAL17292;

XX AC AEAL17292;

XX AC AEAL17292;

XX AC AEAL17292;

XX AC AEAL17292;

XX AC AEAL17292;

DR WPI; 2005-386333/39.
 DR N-PSDB; AEAL17291, AEAL17302.

XX New isolated nucleic acid molecule encoding Golf G proteins, useful for
 PT identifying modulators of G protein coupled receptor activity, or for
 PT diagnosing or treating schizophrenia and other psychiatric disorders.

XX Claim 8; SEQ ID NO 2; 235pp; English.

XX This invention relates to a novel transcriptional variant of the human
 CC GNAL gene that encodes a novel splice variant of the G protein alpha
 CC subunit protein Golf, referred to herein as XLGolf, as well as methods
 CC for identifying modulators of G protein coupled receptors (GPCRs). Note
 CC that the N-terminus of the XLGolf protein is altered compared to Golf
 CC with a different exon 1. Specifically, it refers to contacting the GPCR
 CC with a test compound, and determining GPCR activity, where a change in
 CC activity indicates that the compound is a modulator thereof. The present
 CC invention describes the GPCR as a Gs coupled GPCR that is selected from
 CC dopamine receptor D1, adenosine A2a receptor, and adrenergic beta-2
 CC receptor. Accordingly, the composition and methods are useful for
 CC identifying modulators of GPCR activity, as well as for diagnosing or
 CC treating schizophrenia and other psychiatric disorders. Furthermore, the
 CC pharmaceutical compositions derived thereof exhibit neuroleptic activity
 CC and can be used for gene therapy purposes. This polypeptide sequence is
 CC the human XLGolf protein of the invention.

XX SQ Sequence 458 AA;

Query Match 100.0%; Score 2400; DB 9; Length 458;
 Best Local Similarity 100.0%; Pred. No. 6.3e-200;
 Matches 458; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGLCYSLRPLFLFGPGDDPCAASEPPVEDAQAPALAPVRAAARDTARTLLPRGEGS 60
 DB 1 MGLCYSLRPLFLFGPGDDPCAASEPPVEDAQAPALAPVRAAARDTARTLLPRGEGS 60

QY 61 PACARPKADPKPEKQRTQTEQLSAEREAAKEREAVKEARKVSGIDRMRLDQKRDLDQTH 120
 DB 61 PACARPKADPKPEKQRTQTEQLSAEREAAKEREAVKEARKVSGIDRMRLDQKRDLDQTH 120

QY 121 RLLLLGAGESGKSTIVKQMRILHVNGFNPEEKQKILDIRKNVKDAIVTVSAMSTIIPP 180
 DB 121 RLLLLGAGESGKSTIVKQMRILHVNGFNPEEKQKILDIRKNVKDAIVTVSAMSTIIPP 180

QY 181 VPLANPENQFRSDYIKSIAPITDFEYSQEFDFHVKKLWDDGVKACFERSNEYQLIDCAQ 240
 DB 181 VPLANPENQFRSDYIKSIAPITDFEYSQEFDFHVKKLWDDGVKACFERSNEYQLIDCAQ 240

QY 241 YFLERIDSVSLVDYPTDQDQLLCRVLTSGIFETRFQVDKVNFMFVGVGQDERRKWIQ 300
 DB 241 YFLERIDSVSLVDYPTDQDQLLCRVLTSGIFETRFQVDKVNFMFVGVGQDERRKWIQ 300

QY 301 CFNDVTAIYVAACSSYNMVIREDNNTNRLRESLDLFESINNNRWLRTISIIILFNKQDM 360
 DB 301 CFNDVTAIYVAACSSYNMVIREDNNTNRLRESLDLFESINNNRWLRTISIIILFNKQDM 360

QY 361 LAEKVLGSKIEDYFPEYANYTVPEDATPDAGEDPKVTRAKFFIRDLFLRISTATGDGK 420
 DB 361 LAEKVLGSKIEDYFPEYANYTVPEDATPDAGEDPKVTRAKFFIRDLFLRISTATGDGK 420

QY 421 HCYCPHFTCAVDTENIRRVFNDCRDIIQRMHLKQYELL 458
 DB 421 HCYCPHFTCAVDTENIRRVFNDCRDIIQRMHLKQYELL 458

RESULT 3

ADG74746

XX ID ADG74746 standard; protein; 448 AA.

XX AC ADG74746;

XX DT 22-APR-2004 (first entry)

XX Bostwick RJ, Corradi J, Defay T, Furlong S, Hirata LT, Ravyn V;
 XX Robbins A;

DE Mouse G-protein Gml amino acid sequence.

XX G protein; Gml; G protein-coupled receptor mediated signal transduction;

KW GTP binding site; GTPase site; G protein alpha subunit;

KW signal transduction; G-protein-coupled receptor; mouse; murine.

XX Mus musculus.

XX EPI382613-A1.

XX 21-JAN-2004.

XX 09-JUL-2003; 2003EP-00015519.

XX 16-JUL-2002; 2002JP-00206841.

PR 19-DEC-2002; 2002JP-00367778.

PR 31-MAR-2003; 2003JP-00095955.

XX (SUMO) SUMITOMO CHEM CO LTD.

XX Takahashi Y, Matsumoto Y, Oeda K;

XX WPI; 2004-1111483/12.

DR N-PSDB; ADG74748.

XX New protein useful as a therapeutic or prophylactic agent against a

PT disease caused by an abnormality in a G-protein coupled receptor mediated

PT signal transduction.

XX Claim 1; SEQ ID NO 25; 85pp; English.

XX This invention relates to a novel G protein (Gml). The protein is

CC involved in a G protein-coupled receptor mediated signal transduction.

CC The protein of the invention has a sequence with a high homology with a

CC GTP binding site and a GTPase site conserved among G protein alpha

CC subunits. The protein, the DNA sequence which encodes it and an antibody

CC specifically recognising the protein of the invention may be useful as a

CC therapeutic or prophylactic agent against a disease caused by an

CC abnormality in a G-protein coupled receptor mediated signal transduction.

CC The invention may also be useful for screening for a substance capable of

CC regulating a signal transduction mediated by a G-protein-coupled receptor

CC and a protein. The present sequence is that of the mouse Gml protein

CC which is related to the human Gml protein of the invention.

XX SQ Sequence 448 AA;

Query Match 88.5%; Score 2124; DB 8; Length 448;

Best Local Similarity 91.0%; Pred. No. 6.7e-176; Indels 10; Gaps 3;

Matches 417; Conservative 6; Mismatches 25;

QY 1 MGLCYSLRPLLFSGGDDPCAASEPPVEDAQAPAPALAPVRAAARDTARTLLPRGGE 60

DB 1 MGLCYSLRPLLFSGPETTPCAASEPCAEADQPSAPAPASIPAPA--PVGTLRRGGRI 58

QY 61 PACARPKADPKPKRQTEQLSABEREAAREAVKEARKVSRGIDRLMRDQKRDLOQTH 120

DB 59 VANARPPGE--LQSRRQEQQLRAEREA-----KEARKVSRGIDRLMRDQKRDLOQTH 110

QY 121 RLLLLGSGSKSTIVKQMLHNGFNPEKKQKILDIRNVKDAITVIVSAMSTIIPP 180

DB 111 RLLLLGSGSKSTIVKQMLHNGFNPEKKQKILDIRNVKDAITVIVSAMSTIIPP 170

QY 181 VPLANPENQFRSDYIKSIAPITDPEYQSEFFDHVKLWDDEGVKACFERSNEYQLIDCAQ 240

DB 171 VPLANPENQFRSDYIKSIAPITDPEYQSEFFDHVKLWDDEGVKACFERSNEYQLIDCAQ 230

QY 241 YFLERIDSVSLVDYTPDQDLRLCRVLTSGIFETFRFQVDKVNFMFVGGQDERRKWIQ 300

DB 231 YFLERIDSVSLVDYTPDQDLRLCRVLTSGIFETFRFQVDKVNFMFVGGQDERRKWIQ 290

QY 301 CFNDVTAIIVAACSSYNMVIREDNNTNRLRESLDLFESINWNLRTISIIILFNKQDM 360

DB 291 CFNDVTAIIVAACSSYNMVIREDNNTNRLRESLDLFESINWNLRTISIIILFNKQDM 350

QY 361 LAEKVLAKGSKIIDYFPEYANYTVPEDATPDAGDEPKVTRAKFFIRDLFLRISTATGDGK 420

DB 351 LAEKVLAKGSKIIDYFPEYANYTVPEDATPDAGDEPKVTRAKFFIRDLFLRISTATGDGK 410

QY 421 HVCYPHFTCAVDTENIRRVFNDCRDIIQRMHLKQYELL 458

DB 411 HVCYPHFTCAVDTENIRRVFNDCRDIIQRMHLKQYELL 448

RESULT 4

ADG74747

ID ADG74747 standard; protein; 450 AA.

XX ADG74747;

XX 22-APR-2004 (first entry)

XX Rat G-protein Gml amino acid sequence.

XX G protein; Gml; G protein-coupled receptor mediated signal transduction;

KW GTP binding site; GTPase site; G protein alpha subunit;

KW signal transduction; G-protein-coupled receptor; rat.

XX Rattus norvegicus.

XX EPI382613-A1.

XX 21-JAN-2004.

XX 09-JUL-2003; 2003EP-00015519.

XX 16-JUL-2002; 2002JP-00206841.

PR 19-DEC-2002; 2002JP-00367778.

PR 31-MAR-2003; 2003JP-00095955.

XX (SUMO) SUMITOMO CHEM CO LTD.

XX Takahashi Y, Matsumoto Y, Oeda K;

XX WPI; 2004-1111483/12.

DR N-PSDB; ADG74749.

XX New protein useful as a therapeutic or prophylactic agent against a

PT disease caused by an abnormality in a G-protein coupled receptor mediated

PT signal transduction.

XX Claim 1; SEQ ID NO 26; 85pp; English.

XX This invention relates to a novel G protein (Gml). The protein is

CC involved in a G protein-coupled receptor mediated signal transduction.

CC The protein of the invention has a sequence with a high homology with a

CC GTP binding site and a GTPase site conserved among G protein alpha

CC subunits. The protein, the DNA sequence which encodes it and an antibody

CC specifically recognising the protein of the invention may be useful as a

CC therapeutic or prophylactic agent against a disease caused by an

CC abnormality in a G-protein coupled receptor mediated signal transduction.

CC The invention may also be useful for screening for a substance capable of

CC regulating a signal transduction mediated by a G-protein-coupled receptor

CC and a protein. The present sequence is that of the rat Gml protein which

CC is related to the human Gml protein of the invention.

XX SQ Sequence 450 AA;

Query Match 88.0%; Score 2113; DB 8; Length 450;

Best Local Similarity 90.3%; Pred. No. 6.1e-175;

Matches 415; Conservative 7; Mismatches 26; Indels 12; Gaps 4;

QY 1 MGLCYSLRPLLFSGGDDPCAASEPPVEDAQAP--APALAPVRAAARDTARTLLPRGGE 58

DB 1 MGLCYSLRPLLFSGGDDPCAEDEPCAEADQPSAAPAPAPAPAPA--PVGTLRRGDG 58

QY 59 GSPACARPKADPKPKRQTEQLSABEREAAREAVKEARKVSRGIDRLMRDQKRDLOQ 118

Db 59 RIPASRSPVE--LQNRROEQLRABEREAA-----KEARKVSRGIDRMLRQKRDLLQ 110
Qy 119 THRLLLLGAGSGKSTIVKQMRILHVNQFNPBEKKQKILDIRKNVDAIVTIVSAMSTII 178
Db 111 THRLLLLGAGSGKSTIVKQMRILHVNQFNPBEKKQKILDIRKNVDAIVTIVSAMSTII 170
Qy 179 PPVPLANPENQFSDYIKSTIAPITDREYSQEFFPDHVKKLWDDGKACFERSNEYQIDC 238
Db 171 PPVPLANPENQFSDYIKSTIAPITDREYSQEFFPDHVKKLWDDGKACFERSNEYQIDC 230
Qy 239 AQYFLERIDSVLVDTPTDQDLRLCRVLTSGIFETRQVQDKVNFHMDVGGQDERRKW 298
Db 231 AQYFLERIDSVLVDTPTDQDLRLCRVLTSGIFETRQVQDKVNFHMDVGGQDERRKW 290
Qy 299 IQCFNDVTALIIYVAACSSYNMVRDNTNRLRESLDLPESIWNNRWLRTISILFLNQ 358
Db 291 IQCFNDVTALIIYVAACSSYNMVRDNTNRLRESLDLPESIWNNRWLRTISILFLNQ 350
Qy 359 DMLAEKVLGKSKIEDYFPEYANTVPEDATPDAGDPKVTRAKFFIRDLFLRISTATGD 418
Db 351 DMLAEKVLGKSKIEDYFPEYANTVPEDATPDAGDPKVTRAKFFIRDLFLRISTATGD 410
Qy 419 GKHYCPHFTCAVDTENIRRVFNDCRDIIQRMHLKQYELL 458
Db 411 GKHYCPHFTCAVDTENIRRVFNDCRDIIQRMHLKQYELL 450

RESULT 5
ABB09272
ID ABB09272 standard; protein; 381 AA.
XX
AC ABB09272;
XX
DT 10-JUL-2002 (first entry)
XX
DE G protein-coupled receptor (GPCR) >g-olf SEQ ID NO:18.
XX
KW Target activated nucleic acid biosensor; signalling moiety; GPCR;
KW nucleic acid sensor; detection; engineering; drug optimisation;
KW G protein-coupled receptor.
XX
OS Homo sapiens.
XX
PN WO200222882-A2.
XX
PD 21-MAR-2002.
XX
PF 13-SEP-2001; 2001WO-US028835.
XX
PR 13-SEP-2000; 2000US-0232454P.
XX
PA (ARCH-) ARCHEMIX CORP.
XX
PI Stanton M, Epstein D, Hamaguchi N;
XX
DR WPI; 2002-393977/42.
XX
PT Nucleic acid sensor for detecting target molecule, comprises target
PT molecule activation site and optical signalling unit that changes its
PT optical properties upon allosteric modulation sensor after recognition of
PT target.
XX
PS Example 12; Page 88-89; 144pp; English.
XX
CC The present invention describes a nucleic acid sensor molecule (I)
CC comprising a target molecule activation site comprising a structure that
CC recognises a target molecule and an optical signalling unit including at
CC least one nucleotide coupled to a signalling moiety that changes its
CC optical properties upon allosteric modulation of (I) following
CC recognition of the target molecule. (I) is useful for detecting a target
CC molecule associated with a pathological condition or genetic alteration.
CC (I) is useful for identifying a drug compound, by identifying a nucleic

CC acid biosensor-based molecule profile of target molecules associated with
CC a disease trait in a patient, administering a candidate compound to the
CC patient, and monitoring changes in the profile. Alternately, the method
CC involves identifying a number of pathway target molecules, administering
CC a candidate compound to a patient having a disease trait, and monitoring
CC changes in the structure, level or activity of two or more of the pathway
CC target molecules using (I). The profile of target molecules or the
CC changes in the structure is compared to the profile of a reference
CC healthy or diseased population. (I) is useful in multiple assays, for the
CC detection of target molecule. (I) is also useful in diagnostic
CC applications and drug optimisation. The present sequence represents a G
CC protein-coupled receptor, which is used in an example from the present
CC invention
XX
SQ Sequence 381 AA;
Query Match 75.8%; Score 1819; DB 5; Length 381;
Best Local Similarity 95.0%; Pred. No. 1.9e-149;
Matches 345; Conservative 9; Mismatches 9; Indels 0; Gaps 0;
Qy 96 KEARKVSRGIDRMLRQKRDLLQTHRLLLLGAGSGKSTIVKQMRILHVNQFNPBEKKQK 155
Db 19 KERRRANKKIEKQKQERLAVKATHRLLLLGAGSGKSTIVKQMRILHVNQFNPBEKKQK 78
Qy 156 ILDIRKNVDAIVTIVSAMSTIIPVPLANPENQFSDYIKSTIAPITDREYSQEFFDHVK 215
Db 79 ILDIRKNVDAIVTIVSAMSTIIPVPLANPENQFSDYIKSTIAPITDREYSQEFFDHVK 138
Qy 216 KLWDDGKACFERSNEYQIDCAQYFLERIDSVLVDTPTDQDLRLCRVLTSGIFETR 275
Db 139 KLWDDGKACFERSNEYQIDCAQYFLERIDSVLVDTPTDQDLRLCRVLTSGIFETR 198
Qy 276 FQVDKVNFMHMDVGGQDERRKWIQCFNDVTALIIYVAACSSYNMVRDNTNRLRESLD 335
Db 199 FQVDKVNFMHMDVGGQDERRKWIQCFNDVTALIIYVAACSSYNMVRDNTNRLRESLD 258
Qy 336 LPESIWNNRWLRTISILFLNKQDMLAEKVLGKSKIEDYFPEYANTVPEDATPDAGSD 395
Db 259 LPESIWNNRWLRTISILFLNKQDMLAEKVLGKSKIEDYFPEYANTVPEDATPDAGSD 318
Qy 396 PKVTRAKFFIRDLFLRISTATGDGKHVCYPHFTCAVDTENIRRVFNDCRDIIQRMHLKQY 455
Db 319 PKVTRAKFFIRDLFLRISTATGDGKHVCYPHFTCAVDTENIRRVFNDCRDIIQRMHLKQY 378
Qy 456 ELL 458
Db 379 ELL 381
RESULT 6
ADC09607
ID ADC09607 standard; protein; 381 AA.
XX
AC ADC09607;
XX
DT 18-DEC-2003 (first entry)
XX
DE Human G-protein coupled receptor-related protein, SEQ ID 18.
XX
KW Nucleic acid sensor molecule; ligase; cis-hammerhead; protein kinase;
KW human; G-protein coupled receptor.
XX
OS Homo sapiens.
XX
PN WO2003014375-A2.
XX
PD 20-FEB-2003.
XX
PF 09-AUG-2002; 2002WO-US025319.
XX
PR 09-AUG-2001; 2001US-0311378P.
PR 21-AUG-2001; 2001US-0313932P.
PR 13-SEP-2001; 2001US-00952680.

PR 13-NOV-2001; 2001US-0338186P.
 PR 18-JAN-2002; 2002US-0349959P.
 PR 13-MAR-2002; 2002US-0364486P.
 PR 25-MAR-2002; 2002US-0367991P.
 PR 04-APR-2002; 2002US-0369887P.
 PR 01-MAY-2002; 2002US-0376744P.
 PR 31-MAY-2002; 2002US-0385097P.
 XX (ARCH-) ARCHEMIX CORP.
 XX Stanton M, Epstein D, Hamaguchi N, Kurz M, Keefe T, Wilson C;
 PI Grate D, Marshall KA, Mccauley T, Kurz J;
 XX WPI; 2003-300534/29.
 XX Nucleic acid sensor molecule, for identifying/detecting protein kinase in
 PT a sample, comprises a target modulation domain which recognizes a target
 PT molecule, a linker domain, a catalytic domain, and an optical signal
 PT generator.
 XX
 XX Example 5; SEQ ID NO 18; 423pp; English.
 XX
 CC The present invention relates to nucleic acid sensor molecules (I), which
 CC comprise a target modulation domain that recognizes a target molecule
 CC (TM), a linker domain, a catalytic domain, and an optical signal
 CC generating unit. The catalytic domain comprises a ligase or cis-
 CC hammerhead. (I) are useful for identifying or detecting TM in a sample,
 CC preferably a protein kinase in a sample. Target molecules include
 CC proteins, post-translationally modified forms of proteins, peptides,
 CC nucleic acids, oligosaccharides, nucleotides, metabolites, drugs, toxins,
 CC biohazards, ions, carbohydrates, polysaccharides, hormones, receptors,
 CC antigens, antibodies, viruses, metabolites, co-factors, drugs, dyes,
 CC nutrients, growth factors, cCMP, cAMP or cGMP, protein kinase,
 CC phosphorylated protein kinase, extracellular signal regulated kinase
 CC (ERK), a component or product of mitogen activated protein (MAP) kinase
 CC pathway, a MAP kinase pathway associated protein, an extracellular
 CC component of MAP kinase pathway, a component of ERK1/2 MAP, JNK MAP or
 CC P38 MAP kinase pathway, an endogenous form of MAP kinase (MEK), MAP
 CC kinase kinase, or MAP kinase (MEKK), or RAF kinase, Ras protein,
 CC phosphatase, GTP binding protein, G-protein coupled receptor (GPCR),
 CC cytokine, growth factor, cellular metabolite, small molecule or lysosyme.
 CC (I) are also useful for identifying a modulator of protein kinase
 CC activity. In an example from the invention, nucleic acid sensor molecules
 CC which signal human G-protein coupled receptors e.g. the present sequence,
 CC were obtained.
 XX
 SQ Sequence 381 AA;
 Query Match 75.8%; Score 1819; DB 7; Length 381;
 Best Local Similarity 95.0%; Pred. No. 1.9e-149;
 Matches 345; Conservative 9; Mismatches 9; Indels 0; Gaps 0;
 QY 96 KEARKVSRGIDRMRLDQKRLDQOHLRLLLGAGSGKSTIVKQWRIHVNGENPEEKQK 155
 DB 19 KERREANKKEQKQERLAYKATHRLLLGAGSGKSTIVKQWRIHVNGENPEEKQK 78
 QY 156 ILDIRKNVKDAIVTIVSAMSTIIPVPLANPENFRSDYIKSIAPITDFYSOEFDDHVK 215
 DB 79 ILDIRKNVKDAIVTIVSAMSTIIPVPLANPENFRSDYIKSIAPITDFYSOEFDDHVK 138
 QY 216 KLWDEGVKACFERSNEYQLIDCAQYFLERIDSVSLVDYVPTDQDLRLCRVLTSGIPETR 275
 DB 139 KLWDEGVKACFERSNEYQLIDCAQYFLERIDSVSLVDYVPTDQDLRLCRVLTSGIPETR 198
 QY 276 FOVDKVNFMFDVCGQDERKWTQCFNDVTAILIYVAACSSYNNVIREDDNNTLRSLD 335
 DB 199 FOVDKVNFMFDVCGQDERKWTQCFNDVTAILIYVAACSSYNNVIREDDNNTLRSLD 258
 QY 336 LFSIWNRRWLRTISILFLNKQDLAEKVLAGSKIEDYFPPEYANTVTPEDATPDAGED 395
 DB 259 LFSIWNRRWLRTISILFLNKQDLAEKVLAGSKIEDYFPPEYANTVTPEDATPDAGED 318
 QY 396 PKVTRAKFFIRDLFLRISTATGDKGKYCYHFTCAVDTENIRRVFNDCRDIIQRMHLKQY 455

DB 319 PKVTRAKFFIRDLFLRISTATGDKGKYCYHFTCAVDTENIRRVFNDCRDIIQRMHLKQY 378
 QY 456 ELL 458
 DB 379 ELL 381
 RESULT 7
 ADE61907
 ID ADE61907 standard; protein; 381 AA.
 XX
 AC ADE61907;
 XX 29-JAN-2004 (first entry)
 DE Human Protein P38405, SEQ ID NO 7836.
 XX
 KW Human; pain; neuronal tissue; gene therapy;
 KW spinal segmental nerve injury; chronic constriction injury; CCI;
 KW spared nerve injury; SNI; Chung.
 XX
 OS Homo sapiens.
 XX WO2003016475-A2.
 XX 27-FEB-2003.
 XX 14-AUG-2002; 2002WO-US025765.
 PR 14-AUG-2001; 2001US-0312147P.
 PR 01-NOV-2001; 2001US-0346382P.
 PR 26-NOV-2001; 2001US-0333347P.
 XX (GEHO) GEN HOSPITAL CORP.
 PA (FARB) BAYER AG.
 XX Woolf C, D'urso D, Befort K, Costigan M;
 WPI; 2003-268312/26.
 GENBANK; P38405.
 XX New composition comprising two or more isolated polypeptides, useful for
 PT preparing a medicament for treating pain in an animal.
 XX
 PS Claim 1; Page; 1017pp; English.
 XX
 CC The invention discloses a composition comprising two or more isolated rat
 CC or human polynucleotides or a polynucleotide which represents a fragment,
 CC derivative or allelic variation of the nucleic acid sequence. Also
 CC claimed are a vector comprising the novel polynucleotide, a host cell
 CC comprising the vector, a method for identifying a nucleotide sequence
 CC which is differentially regulated in an animal subjected to pain and a
 CC kit to perform the method, an array, a method for identifying an agent
 CC that increases or decreases the expression of the polynucleotide sequence
 CC that is differentially expressed in neuronal tissue of a first animal
 CC subjected to pain, a method for identifying a compound which regulates
 CC the expression of a polynucleotide sequence which is differentially
 CC expressed in an animal subjected to pain, a method for identifying a
 CC compound that regulates the activity of one or more of the
 CC polynucleotides, a method for producing a pharmaceutical composition, a
 CC method for identifying a compound or small molecule that regulates the
 CC activity in an animal of one or more of the polypeptides given in the
 CC specification, a method for identifying a compound useful in treating
 CC pain and a pharmaceutical composition comprising the one or more
 CC polypeptides or their antibodies. The polynucleotide or the compound that
 CC modulates its activity is useful for preparing a medicament for treating
 CC pain (e.g. spinal segmental nerve injury (Chung), chronic constriction
 CC injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene
 CC therapy). The sequence presented is a human protein (shown in Table 2 of
 CC the specification) which is differentially expressed during pain. Note:
 CC The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic form directly from WIPO at

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CC ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 381 AA;

Query Match 75.8%; Score 1819; DB 7; Length 381;
Best Local Similarity 95.0%; Pred. No. 1.9e-149;
Matches 345; Conservative 9; Mismatches 9; Indels 0; Gaps 0;

Qy 96 KEARKVSRGIDRMRLDQKRDILQQTHRLLLLGAGESGKSTIVKQMRILHVNQFNPEKKQK 155
   || : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 19 KERREANKKIEQLOKERLAYKATHRLLLLGAGESGKSTIVKQMRILHVNQFNPEKKQK 78

Qy 156 ILDIRKNVKDAIVTVSAMSTIIPVPLANPENQFRSDYIKSIAPITDFFEYSQEFFDHVK 215
   ||||| : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 79 ILDIRKNVKDAIVTVSAMSTIIPVPLANPENQFRSDYIKSIAPITDFFEYSQEFFDHVK 138

Qy 216 KLWDEGVKACFERSNEYQLIDCAQYFLERDSVSLVDYTPDQDILLRCVLTSGIFETR 275
   ||||| : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 139 KLWDEGVKACFERSNEYQLIDCAQYFLERDSVSLVDYTPDQDILLRCVLTSGIFETR 198

Qy 276 FQVDKVNFMFDVGQGDERRKWKQCFNDVTALIVAAACSYNNVREDNNTNLRSLD 335
   ||||| : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 199 FQVDKVNFMFDVGQGDERRKWKQCFNDVTALIVAAACSYNNVREDNNTNLRSLD 258

Qy 336 LFESIMNWRNLRTISIILFLNKQDMLAEKVLGASKIEDYFPEYANVTVPEDATPDAGED 395
   ||||| : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 259 LFESIMNWRNLRTISIILFLNKQDMLAEKVLGASKIEDYFPEYANVTVPEDATPDAGED 318

Qy 396 PKVTRAKFFIRDLFLRISTATGDGKHVCYPHFTCAVDTENIRRVFNDRCRDI IQRMHLKQY 455
   ||||| : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 319 PKVTRAKFFIRDLFLRISTATGDGKHVCYPHFTCAVDTENIRRVFNDRCRDI IQRMHLKQY 378

Qy 456 ELL 458
   |||
Db 379 ELL 381

RESULT 8
ADU60726
ID ADU60726 standard; protein; 381 AA.
XX
AC ADU60726;
XX
XX
XX
XX 27-JAN-2005 (first entry)
XX
DE Human G-protein coupled receptor (GPCR) polypeptide #6.
XX
KW Nucleic acid sensor molecule; NASM; biosensor; target molecule;
KW catalytic domain; protein kinase activity; ligase ribozyme;
KW endonucleolytic ribozyme; self-ligating ribozyme; human;
KW G-protein coupled receptor; GPCR; receptor.
XX
OS Homo sapiens.
XX
XX US2004219523-A1.
XX
XX 04-NOV-2004.
XX
XX 09-AUG-2002; 2002US-00215982.
XX
XX 13-SEP-2000; 2000US-0232454P.
XX
XX 09-AUG-2001; 2001US-0311378P.
XX
XX 21-AUG-2001; 2001US-0313932P.
XX
XX 13-SEP-2001; 2001US-00952680.
XX
XX 13-NOV-2001; 2001US-0038186P.
XX
XX 18-JAN-2002; 2002US-0349959P.
XX
XX 13-MAR-2002; 2002US-0364486P.
XX
XX 25-MAR-2002; 2002US-0367991P.
XX
XX 04-APR-2002; 2002US-0369887P.
XX
XX 01-MAY-2002; 2002US-0376744P.
XX
XX 31-MAY-2002; 2002US-0385097P.
XX
XX (STAN/) STANTON M.

```


QY 59 GSPACARPKADKP-KEKQRTQTEQLSAEEREAREAVKEARKVSRGIDRMRLDQKRDQ 117
 Db 355 GLSECTRSLSLSPGKADKPWEERRKQMRKEAIEMRQKADKRSKLIDKQLEEEKWDYM 414
 QY 118 QTHRLLLGAGSGKSTIVKQMRILHVGNGFNP-EKKQKILDIRKNVDAIIVTIVSAMST 176
 Db 415 CTHRLLLGAGSGKSTIVKQMRILHVGNGFNGDSEKATKVQDIKNLKEAIIETIVAAMSN 474
 QY 177 IIPVPLANPENQFRSDYIKSIAPITDPEYSQEFFDHHVKLWDDEGVKACFERSNEYQLI 236
 Db 475 LVPPVELANPENQFRSDYILSVNPNFDPPEFYEHAKEALWDEGVKACFERSNEYQLI 534
 QY 237 DCAQYFLERIDSVSLVDYPTDQDLRLCRVLTSGIFETRFQVDKVNFMFVGGQDERR 296
 Db 535 DCAQYFLDKIDVTKQADYVPSDQDLRLCRVLTSGIFETRFQVDKVNFMFVGGQDERR 594
 QY 297 KWIQCFNDVTAIYVAACSSYNMVIREDNNTNRLRESLDFESIMNWRMLRTISIILFLN 356
 Db 595 KWIQCFNDVTAIYFVVAASSYNMVIREDNNTNRLQELALNLFKSIWNWRMLRTISVILFLN 654
 QY 357 KQDLAEKVLGSKIEDYFPEYANVTVPEDATPDAGEDPKVTRAKFFIRDLFLRISTAT 416
 Db 655 KQDLAEKVLGSKIEDYFPEYARVTPEDATPEFGEDPRVTRAKYFIRDFELRISTAS 714
 QY 417 GDGKHVCYPHFTCAVDTENIRRVFNDCRDIIQRMHLKQYELL 458
 Db 715 GDGRHYCYPHFTCAVDTENIRRVFNDCRDIIQRMHLRQYELL 756

RESULT 13

ID ABP97657
 XX ABP97657 standard; protein; 756 AA.
 AC ABP97657;
 XX 16-MAY-2003 (first entry)
 XX Amino acid sequence of a murine GNAS polypeptide G protein xi-alpha.
 XX GNAS; lymphoma; drug screening; leukemia; wound; inflammation;
 KW immunotherapy; oncogene; vaccine; G protein xi-alpha.
 XX Mus musculus.
 XX WQ2003006688-A2.
 XX 23-JAN-2003.
 XX 15-JUL-2002; 2002WO-EP007853.
 XX 13-JUL-2001; 2001US-00905390.
 PR 24-SEP-2001; 2001WO-US029798.
 XX (UYAA-) UNIV AARHUS.
 XX Pedersen FS, Sorensen AB, Hernandez JM;
 XX WPI; 2003-229494/22.
 DR N-PSDB; AB268699.

Screening drug candidates which can modulate Gnas proteins for treating
 PT lymphoma or leukemia, comprises contacting a cell expressing a GNAS gene
 PT with a candidate drug and determining the effect of the drug on gene
 PT expression.
 XX Disclosure; Page 49; 79pp; English.
 XX The present sequence represents the GNAS polypeptide G protein xi-alpha.
 CC GNAS is a complex locus encoding multiple proteins, and GNAS genes are
 CC implicated in lymphoma and leukemias. The specification describes a
 CC method for screening drug candidates. The method comprises providing a
 CC cell expressing a GNAS gene, adding a drug candidate to the cell, and
 CC determining the effect of the drug candidate on the expression of a GNAS

CC gene. The method is useful for screening drugs which can modulate GNAS
 CC proteins and which can be used to treat lymphomas, leukemia, wounds and
 CC inflammation. Antibodies raised against a GNAS protein are useful in
 CC passive or active immunotherapy, for inhibiting oncogenes, and for
 CC diagnosing lymphoma from blood samples. GNAS proteins may be used as
 CC markers of lymphoma, in situ imaging techniques, in drug screening
 CC assays or by evaluating the effect of drug candidates on a gene or
 CC protein expression profile, and in generating antibodies against the
 CC protein. GNAS genes may be used as probes to determine the number of
 CC copies of the GNAS gene in the genome or to determine the chromosomal
 CC location of the GNAS gene, and as DNA vaccines
 XX
 SQ Sequence 756 AA;

Query Match 65.0%; Score 1559; DB 6; Length 756;
 Best Local Similarity 72.6%; Pred. No. 2.2e-126;
 Matches 292; Conservative 48; Mismatches 60; Indels 2; Gaps 2;
 QY 59 GSPACARPKADKP-KEKQRTQTEQLSAEEREAREAVKEARKVSRGIDRMRLDQKRDQ 117
 Db 355 GLSECTRSLSLSPGKADKPWEERRKQMRKEAIEMRQKADKRSKLIDKQLEEEKWDYM 414
 QY 118 QTHRLLLGAGSGKSTIVKQMRILHVGNGFNP-EKKQKILDIRKNVDAIIVTIVSAMST 176
 Db 415 CTHRLLLGAGSGKSTIVKQMRILHVGNGFNGDSEKATKVQDIKNLKEAIIETIVAAMSN 474
 QY 177 IIPVPLANPENQFRSDYIKSIAPITDPEYSQEFFDHHVKLWDDEGVKACFERSNEYQLI 236
 Db 475 LVPPVELANPENQFRSDYILSVNPNFDPPEFYEHAKEALWDEGVKACFERSNEYQLI 534
 QY 237 DCAQYFLERIDSVSLVDYPTDQDLRLCRVLTSGIFETRFQVDKVNFMFVGGQDERR 296
 Db 535 DCAQYFLDKIDVTKQADYVPSDQDLRLCRVLTSGIFETRFQVDKVNFMFVGGQDERR 594
 QY 297 KWIQCFNDVTAIYVAACSSYNMVIREDNNTNRLRESLDFESIMNWRMLRTISIILFLN 356
 Db 595 KWIQCFNDVTAIYFVVAASSYNMVIREDNNTNRLQELALNLFKSIWNWRMLRTISVILFLN 654
 QY 357 KQDLAEKVLGSKIEDYFPEYANVTVPEDATPDAGEDPKVTRAKFFIRDLFLRISTAT 416
 Db 655 KQDLAEKVLGSKIEDYFPEYARVTPEDATPEFGEDPRVTRAKYFIRDFELRISTAS 714
 QY 417 GDGKHVCYPHFTCAVDTENIRRVFNDCRDIIQRMHLKQYELL 458
 Db 715 GDGRHYCYPHFTCAVDTENIRRVFNDCRDIIQRMHLRQYELL 756

RESULT 14

ID ADQ26060
 XX ADQ26060 standard; protein; 909 AA.
 AC ADQ26060;
 XX 23-SEP-2004 (first entry)
 XX Guanine nucleotide binding protein, alpha stimulating complex locus #2.
 DE BCEC; brain capillary endothelial cell; astrocyte; permeability;
 KW endothelial cell; pro-barrier; PB;
 KW microvascular permeability-modifying disorder;
 KW neurodegenerative disorder; cerebrovascular accident;
 KW Alzheimer's disease; vascular-related dementia;
 KW Creutzfeldt-Jacob disease; bovine spongiform encephalopathy;
 KW Parkinson's disease; brain trauma; multiple sclerosis;
 KW peripheral disorder; septic shock; hepatic encephalopathy;
 KW diabetic hypertension; diabetic microangiopathy; sleeping sickness;
 KW neuropsychiatric disorder; depression; autism; schizophrenia; psychosis;
 KW CNS disorder; brain tumour; epilepsy; migraine; narcolepsy; insomnia;
 KW chronic fatigue syndrome; mountain sickness; AIDS-related dementia;
 KW angiodysplasia-related disorder; proliferative vitreoretinopathy;
 KW rheumatoid arthritis; Crohn's disease; atherosclerosis;
 KW ovarian hyperstimulation; preeclampsia; endometriosis; neovascularisation;
 KW restenosis; balloon angioplasty; scar tissue overproduction;

peripheral vascular disease; hypertension; inflammation; inflammatory vasculitis;
 Reynaud's disease; Reynaud's phenomenon; aneurysm; arterial restenosis;
 thromboembolism; lymphangitis; lymphedema; wound healing; tissue repair;
 ischaemia reperfusion injury; angina; myocardial infarction;
 chronic heart condition; osteoporosis;
 Guanine nucleotide binding protein; alpha stimulating complex locus;
 GNAS.

XX
 XX
 OS Homo sapiens.
 XX
 PN WO2004056386-A2.
 XX
 XX 08-JUL-2004.
 XX
 PF 19-DEC-2003; 2003WO-NL000915.
 XX
 XX 19-DEC-2002; 2002EP-00080503.
 PR
 XX 25-APR-2003; 2003US-046234P.
 PR
 XX (UYLE-) RIJKSUNIV LEIDEN.
 PA
 XX Gaillard PJ, De Boer AG, Brink A;
 PI
 XX WPI; 2004-500264/47.
 DR
 XX
 XX
 PT Modulating the permeability of endothelial cells, useful for treating or
 preventing e.g. neurodegenerative disorders, comprises altering in the
 endothelial cells the activity or the steady-state level of a pro-barrier
 polypeptide.
 PT
 PT
 XX
 XX
 PS Claim 1; SEQ ID NO 14; 222pp; English.
 CC
 CC This sequence represents guanine nucleotide binding protein, alpha
 stimulating complex locus encoded by the GNAS gene. This protein is
 upregulated in BCEC (brain capillary endothelial cells) by physical co-
 culture with astrocytes. This protein sequence may be used in the method
 of the invention for modulating the permeability of endothelial cells.
 CC
 CC The method comprises altering in the endothelial cells the activity or
 the steady-state level of a pro-barrier (PB) polypeptide having an amino
 acid sequence having at least 90% identity with a claimed amino acid
 sequence selected from ADQ26047ADQ26048ADQ26049ADQ26050ADQ26051ADQ26052AD
 Q26053ADQ26054ADQ26055ADQ26056ADQ26057ADQ26058ADQ26059ADQ26060ADQ26061ADQ
 26062ADQ26063ADQ26064ADQ26065ADQ26066ADQ26067ADQ26068ADQ26069ADQ26070ADQ2
 6071ADQ26072ADQ26073ADQ26074ADQ26075ADQ26076ADQ26077ADQ26078ADQ26079ADQ26
 080ADQ26081ADQ26082ADQ26083ADQ26084ADQ26085ADQ26086ADQ26087ADQ26088ADQ260
 89ADQ26090ADQ26091ADQ26092ADQ26093ADQ26094ADQ26095ADQ26096ADQ26097ADQ2609
 8ADQ26099. The PB polypeptides, nucleic acid molecules encoding them
 CC
 CC antagonists or a gene therapy vector comprising an antisense nucleotide
 sequence capable of inhibiting the expression of the nucleotide sequence
 CC
 CC encoding a PB polypeptide, are useful in the manufacture of a composition
 for treating or preventing a microvascular permeability-modifying
 CC
 CC disorder, including neurodegenerative disorders (e.g. cerebrovascular
 CC
 CC accidents, Alzheimer's disease, vascular-related dementia, Creutzfeldt-
 CC
 CC Jacob disease, bovine spongiform encephalopathy, Parkinson's disease,
 CC
 CC brain trauma, multiple sclerosis), peripheral disorders with a CNS
 CC
 CC component (such as septic shock, hepatic encephalopathy, (diabetic)
 CC
 CC hypertension, diabetic microangiopathy or sleeping sickness),
 CC
 CC neuropsychiatric disorders (e.g. depression, autism, schizophrenia and
 CC
 CC other psychoses; other CNS disorders (brain tumours, epilepsy, migraine,
 CC
 CC narcolepsy, insomnia, chronic fatigue syndrome, mountain sickness, or
 CC
 CC AIDS-related dementia); and angiogenesis-related disorders (proliferative
 CC
 CC vitreoretinopathy, rheumatoid arthritis, Crohn's disease,
 CC
 CC atherosclerosis, ovarian hyperstimulation, psoriasis, endometriosis
 CC
 CC associated with neovascularisation, restenosis subsequent to balloon
 CC
 CC angioplasty, scar tissue overproduction, peripheral vascular disease,
 CC
 CC hypertension, inflammatory vasculitides, Reynaud's disease, Reynaud's
 CC
 CC phenomenon, aneurysms, arterial restenosis, thrombophlebitis,
 CC
 CC lymphangitis, lymphedema, wound healing and tissue repair, ischaemia
 CC
 CC reperfusion injury, angina, myocardial infarctions, chronic heart
 CC
 CC conditions, or osteoporosis). The PB polypeptide may also be used in the
 CC
 CC manufacture of a composition for reversibly increasing the microvascular
 CC
 CC permeability in a subject.

SQ Sequence 909 AA;
 Query Match 65.0%; Score 1559; DB 8; Length 909;
 Best Local Similarity 68.6%; Pred. No. 2.9e-126;
 Matches 300; Conservative 49; Mismatches 68; Indels 20; Gaps 4;
 QY 42 RAAARDARTLTPR---GGEGSPACARPADKP-KEKQRTQEQLSAEERAAKEREAVKE 97
 DB 473 RKPQRLNRLNLFVQAFGGCFGRSESPQKASRLKVKVPLAKRQMRKEALEKRAQKR 532
 QY 98 A-RKVSRGIDRLMDQKRDLDQTHRLLLGAGSGSKSTIVKMRILHVNFGNPE----- 150
 DB 533 AEKRSKLDKQLODEKMGVMTCHRLLLGAGSGSKSTIVKMRILHVNFGNFGEGEDP 592
 QY 151 -----EKKQKILDIRKNVDAIVTIVSAMSTIIPVPLANPENQFSDYKSTAPI 201
 DB 593 QAARSNSDGEKATKVQDIKNLKEAETIVAAASNLVPPVELANPENQFSDYKSTAPI 652
 QY 202 TDFEYSQEPFDHVKLWDDDEGVKACFERSNEYQLIDCAQYFLERIDSLSVLTPTDQDL 261
 DB 653 PDFDFPPEFYEHAHALWEDEGVKACFERSNEYQLIDCAQYFLERIDSLSVLTPTDQDL 712
 QY 262 LRCRVLTSGIFETRFQVDKVNPHMFDVGGORDERRKWIQCFNDVTALIIYVAACSSNMVI 321
 DB 713 LRCRVLTSGIFETRFQVDKVNPHMFDVGGORDERRKWIQCFNDVTALIIYVAACSSNMVI 772
 QY 322 REDNNTNRLRESLDLFEFESINNRNRLTISIILFNKQDLMAEKVLAKGSKIEDYFPEYAN 381
 DB 773 REDNNTNRLRESLDLFEFESINNRNRLTISIILFNKQDLMAEKVLAKGSKIEDYFPEYAN 832
 QY 382 YTVPEDATPDAGDDPKVTRAKFPFIRDLFLRISTATGDKGHYCYPHFTCAVDTENIRRVFN 441
 DB 833 YTVPEDATPDAGDDPKVTRAKFPFIRDLFLRISTATGDKGHYCYPHFTCAVDTENIRRVFN 892
 QY 442 DCRDIIQRMHLKOYELL 458
 DB 893 DCRDIIQRMHLKOYELL 909

RESULT 15
 ABM82265
 ID ABM82265 standard; protein; 909 AA.
 AC ABM82265;
 DT 18-NOV-2004 (first entry)
 XX
 DE Tumour-associated antigenic target (TAT) polypeptide PRO83186, SEQ:5829.
 XX
 KW Tumour-associated antigenic target; TAT; human; overexpression; cancer;
 KW
 KW tumour; diagnosis; cell proliferative disorder; breast cancer;
 KW
 KW colorectal cancer; lung cancer; ovarian cancer; liver cancer;
 KW
 KW central nervous system cancer; bladder cancer; pancreatic cancer;
 KW
 KW cervical cancer; melanoma; leukaemia; hybridisation probe;
 KW
 KW chromosome identification; chromosome mapping; gene mapping;
 KW
 KW gene therapy; cytostatic.
 XX
 OS Homo sapiens.
 XX
 XX WO2004030615-A2.
 PN
 XX 15-APR-2004.
 PD
 XX 29-SEP-2003; 2003WO-US028547.
 PF
 XX 02-OCT-2002; 2002US-0414971P.
 PR
 XX (GETH) GENENTECH INC.
 PA
 XX Wu TD, Zhang Z, Zhou Y;
 PI
 XX WPI; 2004-347921/32.
 DR
 XX N-PSDB; ACN40807.

xx New tumor-associated antigenic target polypeptides and nucleic acids,
 PT useful in preparing a medicament for treating or detecting a
 PT proliferative disorder, e.g. breast, lung, colorectal, ovarian or
 PT prostate cancer or tumor.
 xx Claim 12; SEQ ID NO 5829; 7273pp; English.
 xx
 CC The invention relates to human tumour-associated antigenic target (TAT)
 CC polypeptides, and their related nucleic acids. The TAT polypeptides are
 CC overexpressed in cancer tissues compared to normal tissues, and may thus
 CC serve as effective targets for the diagnosis and treatment of cancer in
 CC mammals. The invention also relates to nucleic acid and polypeptide
 CC sequences at least 80% identical to the TAT nucleic acids and
 CC polypeptides; expression vectors and host cells comprising a TAT nucleic
 CC acid; an antibody specific for a TAT polypeptide; a peptide or organic
 CC molecule which binds to a TAT polypeptide; fusion proteins comprising a
 CC TAT polypeptide; and methods and compositions for the treatment or
 CC diagnosis of cancer in mammals. TAT polypeptides, nucleic acids,
 CC antibodies, antagonists, binding molecules and compositions are useful
 CC for diagnosing or treating a cell proliferative disorder associated with
 CC increased TAT expression, particularly cancers such as breast cancer,
 CC colorectal cancer, lung cancer, ovarian cancer, liver cancer, bladder
 CC cancer, pancreatic cancer, cervical cancer, cancers of the central
 CC nervous system, melanoma and leukaemia. TAT nucleic acids may further be
 CC used as hybridisation probes, in chromosome and gene mapping, in
 CC chromosome identification and in gene therapy. The present sequence
 CC represents a TAT polypeptide of the invention
 xx
 SQ Sequence 909 AA;
 Query Match 65.0%; Score 1559; DB 8; Length 909;
 Best Local Similarity 68.6%; Pred. No. 2.9e-126;
 Matches 300; Conservative 49; Mismatches 68; Indels 20; Gaps 4;
 QY 42 RAAARDPARTLLPR--GEGSPACAPKADP-KEKRQTEQLSAEEREAAKEREAVKE 97
 DB 473 RKPQNLRLNLFVQAFGFCGRSESPQKASRSILKVKVPLAEKRQMRKEALEKRAQR 532
 QY 98 A-RKVSIGDIRMLRDQRDIQQTHRLLLLGAGSGSKSTIVKQMRILHVNQFNPE----- 150
 DB 533 AEKRSKLIDKQLQDERKMGYMCYTHRLLLLGAGSGSKSTIVKQMRILHVNQFNQGEEDP 592
 QY 151 -----EKKOKILDIRKNVDAIVTIVSAMSTIIPVPLANPENQFSDYIKSIAP 201
 DB 593 QAARNSDGEKATKVDIKNKEALETIVAASNLVPPVELANPENQFVDYILSVNMV 652
 QY 202 TDFEYSQEFEDHVKKLWDEGVKACFERSNEYQLIDCAQYFLERIDSVLSVDTPTDQDL 261
 DB 653 PDFDFPPEFYEHAHALWEDEGVACVRSNEYQLIDCAQYFLDKIDVIKQADYVPSDQDL 712
 QY 262 LRCRVLTSGIFETRFQVDKYNFMFDVGGQDERRKWKIQCFNDVTAILIYVACSSYNMVI 321
 DB 713 LRCRVLTSGIFETRFQVDKYNFMFDVGGQDERRKWKIQCFNDVTAILIYVASSYNMVI 772
 QY 322 REDNNTNRLRESLDLPESIWNNRWLRTISILFNKODMLAEKVLACKSKIEDYFPEYAN 381
 DB 773 REDNNTNRLQALNLFASIWNNRWLRTISVILFNKODMLAEKVLACKSKIEDYFPEFAR 832
 QY 382 YTVPEPATPDAGDPKVKTRAKFFIRDLFLRISTATGDKHYCYPHFTCAVDTENIRRVFN 441
 DB 833 YTVPEPATPDGDPKVKTRAKFYIRDEFIRISTASGDGRHYCYPHFTCAVDTENIRRVFN 892
 QY 442 DCRDIITQRMHLKQYELL 458
 DB 893 DCRDIITQRMHLRQYELL 909

Search completed: March 2, 2006, 19:32:17
 Job time : 145.364 secs

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OM protein - protein search, using sw model

Run on: March 2, 2006, 19:30:27 ; Search time 27.1616 Seconds
(without alignments)
1622.414 Million cell updates/sec

Title: US-10-618-320A-1
Perfect score: 2400
Sequence: 1 MGLCYSLRLLFGPGDDPC.....VFNDCRDIQRMHLKQYELL 458
Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues
Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 80.*
1: pir1.*
2: pir2.*
3: pir3.*
4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed; and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1819	75.8	381	2 I53271	G-protein alpha-ol
2	1548	64.5	846	2 S52418	GTP-binding regula
3	1530	63.7	377	1 RGMSA1	GTP-binding regula
4	1529.5	63.7	380	1 RGHUA1	GTP-binding regula
5	1527	63.6	379	1 RGXUA	GTP-binding regula
6	1525.5	63.6	394	2 S33458	GTP-binding regula
7	1525	63.5	395	1 RGHUA2	GTP-binding regula
8	1522.5	63.4	394	1 RGMSA2	GTP-binding regula
9	1520.5	63.4	394	1 RGHVAE	GTP-binding regula
10	1520.5	63.4	394	1 RGHVA2	GTP-binding regula
11	1520.5	63.4	394	1 RGRVA2	GTP-binding regula
12	1518	63.2	397	1 RGPQA2	GTP-binding regula
13	1513.5	63.1	394	1 RBOGA	GTP-binding regula
14	1460	60.8	419	2 S34421	GTP-binding regula
15	1413	58.9	376	2 S27015	GTP-binding regula
16	1398	58.2	382	1 RGFPA5	GTP-binding regula
17	1397.5	58.2	335	2 JH0813	GTP-binding regula
18	1384.5	57.7	385	1 RGFPA1	GTP-binding regula
19	1292	53.8	375	2 T37245	GTP-binding regula
20	1278.5	53.3	385	2 D87723	protein R06A10.2
21	1270.5	52.9	379	2 A42964	guanine nucleotide
22	739.5	30.8	353	2 S34347	GTP-binding regula
23	725.5	30.2	355	2 T15288	hypothetical prote
24	721	30.0	354	2 S27014	GTP-binding regula
25	720.5	30.0	359	2 S45699	GTP-binding regula
26	719.5	30.0	359	1 RGMSQ	GTP-binding regula
27	717.5	29.9	359	2 S71963	GTP-binding protei
28	715	29.8	354	1 RGFPO1	GTP-binding regula
29	715	29.8	354	2 S24352	gustducin - rat

ALIGNMENTS

RESULT 1

I53271
G-protein alpha-olf subunit - human
C:Species: Homo sapiens (man)
C:Date: 31-May-1996 #sequence_revision 31-May-1996 #text_change 09-Jul-2004
C:Accession: I53271
R:Zigman, J.M.; Westermarck, G.T.; LaMendola, J.; Boel, E.; Steiner, D.F.
Endocrinology 133, 2508-2514, 1993
A:Title: Human G(olf) alpha: complementary deoxyribonucleic acid structure and expression
A:Reference number: I53271; MUID:94062616; PMID:843272
A:Accession: I53271
A:Status: preliminary;
A:Molecule type: mRNA
A:Residues: 1-381 <RES>
A:Cross-references: UNIPROT:P38405; UNIPARC:UPI0000001246; GB:L10665; NID:g182967; PIDN:1
A:Superfamily: GTP-binding regulatory protein Gs alpha chain
C:Keywords: GTP binding; nucleotide binding; P-loop
F:49-56/Region: nucleotide-binding motif A (P-loop)
F:279-282/Region: GTP-binding NKXD motif

Query Match 75.8%; Score 1819; DB 2; Length 381;
Best Local Similarity 95.0%; Pred. No. 1e-108;
Matches 345; Conservative 9; Mismatches 9; Indels 0; Gaps 0;

QY	96	KEARKVSRGIDRMLRDKRDLOQTHRELLLGAGESGKSTIVKQMRILHVNQFNPEKKOK	155
DB	19	KERREANKKIEKQLQKERLAYKATHRELLLGAGESGKSTIVKQMRILHVNQFNPEKKOK	78
QY	156	ILDIRKNVKDAIVTVISANSTIIPVPLANPENQFRSDYIKSIAPITDFEYSQEFDFHVK	215
DB	79	ILDIRKNVKDAIVTVISANSTIIPVPLANPENQFRSDYIKSIAPITDFEYSQEFDFHVK	138
QY	216	KLWDEGVKACERSNEYOLIDCAQYFLERISVLSVDTPTDQDLLRCRLVLTSGIFETR	275
DB	139	KLWDEGVKACERSNEYOLIDCAQYFLERISVLSVDTPTDQDLLRCRLVLTSGIFETR	198
QY	276	FQVDKVNFMFMDVGGQDERRKWIQCFNDVTALIIYVACSSYNMVIREDNNTNRLRESLD	335
DB	199	FQVDKVNFMFMDVGGQDERRKWIQCFNDVTALIIYVACSSYNMVIREDNNTNRLRESLD	258
QY	336	LFESIWNNRWLRTISILFLNKKQDLAEKVLAKGSKIEDYFPPEYANTVTPEDATPDAGED	395
DB	259	LFESIWNNRWLRTISILFLNKKQDLAEKVLAKGSKIEDYFPPEYANTVTPEDATPDAGED	318
QY	396	PKVTRAKFIRDLFLRISTATGDKHYCYPHFTCAVDENIRRVFVNDCRDIIQRMHLKQY	455
DB	319	PKVTRAKFIRDLFLRISTATGDKHYCYPHFTCAVDENIRRVFVNDCRDIIQRMHLKQY	378
QY	456	ELL 458	
DB	379	ELL 381	

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RESULT 2

S52418
GTP-binding regulatory protein Gs alpha-XL chain - rat
N;Alternate names: G protein XL-alpha-s
C;Species: Rattus norvegicus (Norway rat)
C;Date: 14-Jul-1995 #sequence_revision 10-Nov-1995 #text_change 02-Feb-2001
C;Accession: S52418
R;Kehlenbach, R.H.; Matthey, J.; Huttner, W.B.
Nature 372, 804-809, 1994
A;Title: XL-alpha-s is a new type of G protein.
A;Reference number: S52418; MUID:95089824; PMID:7997272
A;Accession: S52418
A;Molecule type: mRNA
A;Residues: 1-846 <KEH>
A;Cross-references: UNIPARC:UPI000017C91P; EMBL:X84047; PIDN:CAA58866.1; PI
R;Kehlenbach, R.H.; Matthey, J.; Huttner, W.B.
Nature 375, 253, 1995
A;Title: Correction: XLalphas is a new type of G protein.
A;Reference number: S58911
A;Contents: annotation; assignment of start_codon
A;Note: experimental data from this paper suggest that the translation is initiated at P
C;Keywords: GTP binding; nucleotide binding; P-loop; signal transduction
F;132-846/Product: GTP-binding regulatory protein Gs alpha-XL chain #status experimental
F;499-506/Region: nucleotide-binding motif A (P-loop)
F;744-747/Region: GTP-binding NKXD motif

Query Match 64.5%; Score 1548; DB 2; Length 846;
Best Local Similarity 70.2%; Pred. No. 5.3e-91;
Matches 292; Conservative 47; Mismatches 61; Indels 16; Gaps 2;

QY	59	GSFACAPKADKP-KEKQRTQELSAEEREAAKEREAVKEARKVSGIDRMRLDQKRDQ 117
DB	431	GLSECTRSLSGKADPMEERRKQMRKEAMERQKADKRSKLIDKQLEEEKNDY 490
QY	118	QTHRLLLLAGESGKSTIVKQMLILHVGNGFPE-----EKKQKILDIRKN 162
DB	491	CTHRLLLLAGESGKSTIVKQMLILHVGNGEGGEDPQAARSNDGEKATKQVQIKNN 550
QY	163	VKDAIVTVSAMSTIIPVPLANPENQFRSDYTKSAPITDPYSQEFDFHVKLWDEG 222
DB	551	LKEAETIVAAGNLVPPVELANPENQFRVDYILSVNVPNFPDFPEFVEHAKLWDEG 610
QY	223	VKACFERSNEYQLIDCAQYFLERIDSVLVDYPTDQDLRLCRVLTSGIFETRFQVDKN 282
DB	611	VRACYERSNEYQLIDCAQYFLDKIDVIKQADYVPSDQDLPRCRVLTSGIFETKQVDKN 670
QY	283	FHMFVGGQDERRKWTQCFNDVTAIYVAACSSYNNVIREDNNTNRLRESLDLPSIWN 342
DB	671	FHMFVGGQDERRKWTQCFNDVTAIYVVAASSYNNVIREDNQTNRLQEQALNLFKSIWN 730
QY	343	NRWLRTISIILFNKQDMLAEKVLGSKIEDYFPEYANYTVPEPATPDAGEDPKVTRAK 402
DB	731	NRWLRTISVILFNKQDMLAEKVLGSKIEDYFPEFARYTTPEDATPEPGEDPRVTRAK 790
QY	403	FFTRDLFLRISTATGDKGHYCYPHFTCAVDTEINRVFNDRCRDIIOHMLKQVELL 458
DB	791	YFIRDFELRISTASGDRGHYCYPHFTCAVDTEINRVFNDRCRDIIOHMLKQVELL 846

RESULT 3

RGMSAL
GTP-binding regulatory protein Gs alpha-S1 chain (adenylate cyclase-stimulating) - mouse
N;Alternate names: guanine nucleotide binding protein Gs alpha-S1 chain; heterotrimeric
C;Species: Mus musculus (house mouse)
C;Date: 31-Dec-1992 #sequence_revision 31-Dec-1992 #text_change 09-Jul-2004
C;Accession: A25889
R;Sullivan, K.A.; Liao, Y.C.; Alborzi, A.; Beiderman, B.; Chang, F.H.; Masters, S.B.; Le
Proc. Natl. Acad. Sci. U.S.A. 83, 6687-6691, 1986
A;Title: Inhibitory and stimulatory G proteins of adenylate cyclase: cDNA and amino acid
A;Reference number: A94123; MUID:86313643; PMID:3092218
A;Accession: A25889
A;Molecule type: mRNA

A;Residues: 1-377 <SUL>

A;Cross-references: UNIPROT:P04894; UNIPARC:UPI000016CDAC; GB:M13964; NID:G193652; PIDN:AA
C;Comment: The G proteins are a family of guanine nucleotide-binding proteins that relay
ains. The beta and gamma chains, required for GTPase activity, appear to be common to all
ase; it is specific for each type of G protein.

C;Comment: The Gs alpha chain is specific for G protein that is responsible for transduct
xigic stimuli.

C;Superfamily: GTP-binding regulatory protein Gs alpha chain

C;Keywords: alternative splicing; GTP binding; heterotrimer; nucleotide binding; P-loop;
F;45-52/Region: nucleotide-binding motif A (P-loop)

F;275-278/Region: GTP-binding NKXD motif

F;51/Binding site: GTP (Lys) #status predicted

F;184/Modified site: ADP-ribosylarginine (Arg) (by cholera toxin) #status predicted

Query Match 63.7%; Score 1530; DB 1; Length 377;

Best Local Similarity 76.9%; Pred. No. 2.7e-90;

Matches 279; Conservative 45; Mismatches 39; Indels 0; Gaps 0;

QY	96	KEARKVSGIDRMRLDQKRDLOOQTHRLLLLAGESGKSTIVKQMLILHVGNGPBEKKOK 155
DB	15	KAQREANKKIEKQLOKQDKQVYRATHRLLLLAGESGKSTIVKQMLILHVGNGDEKATK 74

QY	156	ILDIRKNVKDAIVTVSAMSTIIPVPLANPENQFRSDYKSIKSIAPITDFEYSQEFDFHVK 215
DB	75	VQDIKNKLKEAETIVAAGNLVPPVELANPENQFRVDYILSVNMLPNDFPPEFVEHAK 134

QY	216	KLWDEGVKACFERSNEYQLIDCAQYFLERIDSVLSVDYPTDQDLRLCRVLTSGIFETR 275
DB	135	ALWDEGVKACFERSNEYQLIDCAQYFLDKIDVIKQADYVPSDQDLRLCRVLTSGIFETR 194

QY	276	FOVDKVNPFHMFVGGQDERRKWTQCFNDVTAIYVAACSSYNNVIREDNNTNRLRESLD 335
DB	195	FOVDKVNPFHMFVGGQDERRKWTQCFNDVTAIYVVAASSYNNVIREDNQTNRLQEQALN 254

QY	336	LFESINNRNLRTISIILFNKQDMLAEKVLGSKIEDYFPEYANYTVPEPATPDAGED 395
DB	255	LFKSIWNRNLRTISIILFNKQDMLAEKVLGSKIEDYFPEFARYTTPEDATPEPGED 314

QY	396	PKVTRAKFPIRLFLRISTATGDKGHYCYPHFTCAVDTEINRVFNDRCRDIIOHMLKQY 455
DB	315	PRVTRAKFPIRDFLRLRISTASGDRGHYCYPHFTCAVDTEINRVFNDRCRDIIOHMLROY 374

QY	456	ELL 458
DB	375	ELL 377

RESULT 4

RGHUAL

GTP-binding regulatory protein Gs alpha chain (adenylate cyclase-stimulating), splice for
N;Alternate names: guanine nucleotide binding protein Gs alpha-S1 chain; heterotrimeric
C;Species: Homo sapiens (man)
C;Date: 31-Dec-1990 #sequence_revision 31-Dec-1990 #text_change 31-Dec-2004
C;Accession: C31927; D31927; B24366

R;Kozasa, T.; Itoh, H.; Tsukamoto, T.; Kaziro, Y.

Proc. Natl. Acad. Sci. U.S.A. 85, 2081-2085, 1988

A;Title: Isolation and characterization of the human G-s-alpha gene.

A;Reference number: A31927; MUID:88176890; PMID:3127824

A;Accession: C31927

A;Molecule type: DNA

A;Residues: 1-71,73-380 <K023>

A;Cross-references: UNIPROT:P04895; UNIPROT:Q14433; UNIPARC:UPI000004D203; GB:M21142; DDI

A;Note: splice form 3

A;Accession: D31927

A;Molecule type: DNA

A;Residues: 1-380 <K024>

A;Cross-references: UNIPARC:UPI00000001248; GB:M21142; DDBJ:J03647; NID:G183402; PIDN:AAA

A;Note: splice form 4

R;Mattera, R.; Codina, J.; Crozat, A.; Kidd, V.; Woo, S.L.C.; Birnbaumer, L.

FEBS Lett. 206, 36-42, 1986

A;Title: Identification by molecular cloning of two forms of the alpha-subunit of the hun

A;Reference number: A24366; MUID:87005246; PMID:3093273

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rase; it is specific for each type of G protein.
C;Superfamily: GTP-binding regulatory protein Gs alpha chain
C;Keywords: alternative splicing; blocked amino end; GTP binding; heterotrimer; lipoprot
F;2-379/Product: GTP-binding regulatory protein Gs alpha chain #status predicted <MAT>
F;47-54/Region: nucleotide-binding motif A (P-loop)
F;277-280/Region: GTP-binding NKXD motif
F;2/Modified site: myristylated amino end (Gly) (in mature form) #status predicted
F;3/Binding site: palmitate (Cys) (covalent) #status predicted
F;186/Modified site: ADP-ribosylarginine (Arg) (by cholera toxin) #status predicted

Query Match      63.6%; Score 1527; DB 1; Length 379;
Best Local Similarity 76.4%; Pred. No. 4.2e-90;
Matches 281; Conservative 43; Mismatches 44; Indels 0; Gaps 0;

Qy    91 EREAVKEARKVSRGIDRMLRDQKDLQOTHRLLLLLGAGESGKSTIVKOMRIILHVGFNPE 150
Db    12 QRNEEKVQRETNNKKIEKQLQDKQVYRATHRLLLLLGAGESGKSSIVKOMRIILHVGFNAE 71

Qy    151 EKKOKILDIRKNVDIAVTIIVSAMSITIIPVPPLANPENQFRSDYIKSIAPITDFFEYSOE 210
Db    72 EKTKVQDIQKNIKEAETIIVTAMGNLSPPVVLNPNQFRIDIYLNLPNYKDFESPEF 131

Qy    211 PDHVKKLWDDSGVCACFERSNEYQLIDCAQYFLERIDSLSLVDTPTDQDLRCRLVTSG 270
Db    132 YEHTKLTDQDSGVGRACYERSNEYQLIDCAQYFLDXIDIVKQNDYTPSQDOLLRCRLVTSG 191

Qy    271 IFETRFOVDKVNPFMFVGGQDRERRKWIQCNDVTAIYYAACSSYNMVIREDNNTNRL 330
Db    192 IFETFPQVKVNFMFVGGQDRERRKWIQCNDVTALIFVVASSSYNMVIREDNHTNRL 251

Qy    331 RESLDLPESIWNNRWLRTISILFLNKODMLAEKVLAGSKIEDYPPEYANTYTPEDATP 390
Db    252 QEALNFLKSIWNNRWLRTISVILFNKODLLAEKVNAKSIEDYPPEARYTTTPDATP 311

Qy    391 DAGBDPKVTRAKFIIRDLFLEISTATGKGKYCYPHFTCAVDTENIRRVFNDCRDIQRM 450
Db    312 EVGEDPVRTRAKYPIRDEFLRAISTAGSGDRHYCYPHFTCAVDTENIRRVFNDCRDIQRM 371

Qy    451 HLKOYEELL 458
Db    372 HLRQYEELL 379

RESULT 6
S33458
GTP-binding regulatory protein Gs alpha chain - dog
C;Species: Canis lupus familiaris (dog)
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 09-Jul-2004
C;Accession: S33458
R;Ishikawa, Y.; Homcy, C.J.
submitted to the EMBL Data Library, June 1992
A;Description: cDNA sequence for alpha subunit of stimulatory guanine nucleotide binding
A;Reference number: S33458
A;Accession: S33458
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-394 <ISH>
A;Cross-references: UNIPROT:P04895; UNIPARC:UPI0000001247; EMBL:Z12168; NID:g311336; PID:
C;Superfamily: GTP-binding regulatory protein Gs alpha chain
C;Keywords: GTP binding; nucleotide binding; P-loop
F;47-54/Region: nucleotide-binding motif A (P-loop)
F;292-295/Region: GTP-binding NKXD motif

Query Match      63.6%; Score 1525.5; DB 2; Length 394;
Best Local Similarity 73.6%; Pred. No. 5.4e-90;
Matches 282; Conservative 44; Mismatches 42; Indels 15; Gaps 1;

Qy    91 EREAVKEARKVSRGIDRMLRDQKDLQOTHRLLLLLGAGESGKSTIVKOMRIILHVGFNPE 150
Db    12 QRNEEKAQRANKKIEKQLQDKQVYRATHRLLLLLGAGESGKSTIVKOMRIILHVGFNCE 71

Qy    151 -----EKKOKILDIRKNVDAIVTIVSAMSTIIIPVPPLANPENQFRSDYI 195

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Db 72 GGBEDPQAARSNDGKATKVQDIKNLKEAETIVAAMSLNLPVPELANPENQFRVDYI 131

Qy 196 KSTAPITDFEYSQFFDHVKLLWDDEGVKACFERSNEYQLIDCAQYFLERIDSVSLVDYT 255

Db 132 LSVNVPDFPFPEFYEHAKLWDEGVACYSERSNEYQLIDCAQYFLDKIDVIKQADYV 191

Qy 256 PTQDLRLCRVLTSGIFETRFQVDKVNFMFDVGGQDRERRKWTQCFNDVTALIIYVAACS 315

Db 192 PSODLLRCRVLTSGIFETRFQVDKVNFMFDVGGQDRERRKWTQCFNDVTALIFVASS 251

Qy 316 SYNVMIREDNNTNRLRESLDLFPESIMNRLRTISILFLNKQDMLAEKVLACKSKIEDY 375

Db 252 SYNVMIREDNQTNRLQALNLFKSIWNNRLRTISVILFNKQDMLAEKVLACKSKIEDY 311

Qy 376 FPEVANYTVPEDATPDAGEDPKVTRAKFFIRDLFLRISTATGDKHKYCYPHFTCAVDTEN 435

Db 312 FPEFARYTTPEDATPEGEDPRVTRAKYFIRDFLRISTASDGRHYCYPHFTCAVDTEN 371

Qy 436 IRRVFNDCRDIIORMHLKQYELL 458

Db 372 IRRVFNDCRDIIORMHLKQYELL 394

RESULT 7

RGHUA2

GTP-binding regulatory protein Gs alpha chain (adenylate cyclase-stimulating), splice form 1

N;Alternate names: guanine nucleotide binding protein Gs alpha-S2 chain; heterotrimeric N;Contains: GTP-binding regulatory protein Gs alpha chain, splice form 1

C;Species: Homo sapiens (man)

C;Date: 31-Dec-1990 #sequence revision 15-Jun-1996 #text_change 09-Jul-2004

C;Accession: B31927; A24366; S02122; A25919

R;Kozasa, T.; Itoh, H.; Tsukamoto, T.; Kaziro, Y.

Proc. Natl. Acad. Sci. U.S.A. 85, 2081-2085, 1988

A;Title: Isolation and characterization of the human G-s-alpha gene.

A;Reference number: A31927; MUID:98176890; PMID:3127824

A;Accession: B31927

A;Molecule type: DNA

A;Residues: 1-395 <KOZ2>

A;Cross-references: UNIPROT:Q96H70; UNIPARC:UPI0000004D202; GB:M21142; DDBJ:J03647; NID:9

A;Note: splice form 2

A;Accession: A31927

A;Molecule type: DNA

A;Residues: 1-86,88-395 <KOZ1>

A;Cross-references: UNIPARC:UPI0000001247; GB:M21142; DDBJ:J03647; NID:g183402; PIDN:AAA

A;Note: splice form 1

R;Mattera, R.; Codina, J.; Crosat, A.; Kidd, V.; Woo, S.L.C.; Birnbaumer, L.

FEBS Lett. 206, 36-42, 1986

A;Title: Identification by molecular cloning of two forms of the alpha-subunit of the hu

A;Reference number: A24366; MUID:87005246; PMID:3093273

A;Accession: A24366

A;Molecule type: mRNA

A;Residues: 1-86,88-395 <MAT>

A;Cross-references: UNIPARC:UPI0000001247; EMBL:X04408; NID:g31914; PIDN:CAA27996.1; PID

R;Harris, B.A.

Nucleic Acids Res. 16, 3585, 1988

A;Title: Complete cDNA sequence of a human stimulatory GTP-binding protein alpha subunit

A;Reference number: S02122; MUID:88233954; PMID:3131741

A;Accession: S02122

A;Molecule type: mRNA

A;Residues: 1-5,'T',7-86,88-395 <HAR>

A;Cross-references: UNIPARC:UPI000016AA01; EMBL:X07036; NID:g31951; PIDN:CAA30084.1; PID

R;Bray, P.; Carter, A.; Simons, C.; Guo, V.; Puckett, C.; Kamholz, J.; Spiegel, A.; Nire

Proc. Natl. Acad. Sci. U.S.A. 83, 8893-8897, 1986

A;Title: Human cDNA clones for four species of G-alpha-s-signal transduction protein.

A;Reference number: A25919; MUID:87067419; PMID:3024154

A;Accession: A25919

A;Molecule type: mRNA

A;Residues: 12-230,'Q',232-395 <BRA>

A;Cross-references: UNIPARC:UPI000016A9C8; GB:M14631; NID:g183416; PIDN:AAAS2583.1; PID:

C;Note: The authors translated the codon CAA for residue 221 as Glu

C;Comment: The G proteins are a family of guanine nucleotide-binding proteins that relay

ains. The beta and gamma chains, required for GTPase activity, appear to be common to al

rase; it is specific for each type of G protein.

C;Comment: The Gs alpha chain is specific for G protein that is responsible for transduct

rgic stimuli.

C;Comment: See also PIR:RGHUA1.

C;Genetics:

A;Gene: GDB:GNAS1; GNAS

A;Cross-references: GDB:120628; OMIM:139320

A;Map position: 20q13.2-20q13.3

A;Introns: 47/1; 71/2; 86/2; 105/3; 145/3; 178/2; 196/3; 221/2; 241/1; 281/2; 325/1; 347/

C;Superfamily: GTP-binding regulatory protein Gs alpha chain

C;Keywords: alternative splicing; blocked amino end; GTP binding; heterotrimer; lipoprote

F;2-395/Product: GTP-binding regulatory protein Gs alpha chain, splice form 2 #status pr

F;2-86,88-395/Product: GTP-binding regulatory protein Gs alpha chain, splice form 1 #stat

F;47-54/Region: nucleotide-binding motif A (P-loop)

F;293-296/Region: GTP-binding NKXD motif

F;2/Modified site: myristylated amino end (Gly) (in mature form) #status predicted

F;3/Binding site: myristylated (Cys) (covalent) #status predicted

F;202/Modified site: ADP-ribosylarginine (Arg) (by cholera toxin) #status predicted

Query Match 63.5%; Score 1525; DB 1; Length 395;

Best Local Similarity 73.4%; Pred. No. 5,9e-90;

Matches 282; Conservative 44; Mismatches 42; Indels 16; Gaps 1;

Qy 91 EREAVKEARKVSGIDRMRLRQKDLQOHTHLLGAGSGSKSTIVKQMRILHVNQFNPE 150

Db 12 QRNEEKAQREANKTEKQLQDKQVYVRATHRLLLGAGSGSKSTIVKQMRILHVNQFNGE 71

Qy 151 -----EKQKILDIRKNVKDAIVTVSAMSTIIIPVPLANPENQFRSDY 194

Db 72 GGEEDPQAARSNDGSEKATKVQDIKNLKEAETIVAAMSLNLPVPELANPENQFRVDY 131

Qy 195 IKSIAPITDFEYSQFFDHVKLLWDDEGVKACFERSNEYQLIDCAQYFLERIDSVSLVDY 254

Db 132 ILSVMNVPDFPFPEFYEHAKLWDEGVACYSERSNEYQLIDCAQYFLDKIDVIKQADY 191

Qy 255 TPTDQDLRLCRVLTSGIFETRFQVDKVNFMFDVGGQDRERRKWTQCFNDVTALIIYVAAC 314

Db 192 VPSDQDLRLCRVLTSGIFETRFQVDKVNFMFDVGGQDRERRKWTQCFNDVTALIIFWAS 251

Qy 315 SYNVMIREDNNTNRLRESLDLFPESIMNRLRTISILFLNKQDMLAEKVLACKSKIED 374

Db 252 SSYNVMIREDNQTNRLQALNLFKSIWNNRLRTISVILFNKQDMLAEKVLACKSKIED 311

Qy 375 YPEFANYTVPEDATPDAGEDPKVTRAKFFIRDLFLRISTATGDKHKYCYPHFTCAVDTE 434

Db 312 YPEFARYTTPEDATPEGEDPRVTRAKYFIRDFLRISTASDGRHYCYPHFTCAVDTE 371

Qy 435 NIRRVFNDCRDIIORMHLKQYELL 458

Db 372 NIRRVFNDCRDIIORMHLKQYELL 395

RESULT 8

RGHUA2

GTP-binding regulatory protein Gs alpha-S2 chain (adenylate cyclase-stimulating) - mouse

N;Alternate names: guanine nucleotide binding protein Gs alpha-S2 chain; heterotrimeric

C;Species: Mus musculus (house mouse)

C;Date: 31-Dec-1992 #sequence_revision 31-Dec-1992 #text_change 19-Jan-2001

C;Accession: S03075

R;Hall, T.; Harris, B.A.

FEBS Lett. 224, 365-371, 1987

A;Title: Identification of the lesion in the stimulatory GTP-binding protein of the unco

A;Reference number: S03075; MUID:88083563; PMID:2826231

A;Accession: S03075

A;Molecule type: mRNA

A;Residues: 1-394 <RAL>

A;Cross-references: UNIPARC:UPI0000054C7A; GB:Y00703; NID:g51127; PIDN:CAA68695.1; PID:g

C;Comment: The G proteins are a family of guanine nucleotide-binding proteins that relay

ains. The beta and gamma chains, required for GTPase activity, appear to be common to al

rase; it is specific for each type of G protein.

C;Comment: The Gs alpha chain is specific for G protein that is responsible for transduct

rgic stimuli.

C;Superfamily: GTP-binding regulatory protein Gs alpha chain

C;Keywords: alternative splicing; blocked amino end; GTP binding; heterotrimer; lipoprote

Qy	91	EREAVTEARKVSRGIDRLMLDQKRDLOOQTHRLLLLGAGESGKSTIVKQMRILHVN	150
Db	12	QRNEEKAQREANKKIEKQLOKDQKVYRATHRLLLLGAGESGKSTIVKQMRILHVN	71
Qy	151	-----EKKQKILDIRKVNKDAIVTVISAMSTIIPVPLANPENQFRSDYI	195
Db	72	GGEEDPQAARNSDGEKATKVDQIKNNLKEAETIIVAAMSNLVPVELANPENQFRVDYI	131
Qy	196	KSIAPITDFBSYQBFDFHVKKLWDEGVKACFERSNEYQLIDCAQYFLERIDSV	255
Db	132	LSVMNVNFPDFPFYEYHAKALWDEGVACFERSNEYQLIDCAQYFLDKIDVI	191
Qy	256	PTDQLLRCRLVTSGIFETRFQVDKVNPFMDVGQDERRRKAQICFNDVTAIL	315
Db	192	PSDQLLRCRLVTSGIFETRFQVDKVNPFMDVGQDERRRKAQICFNDVTAIL	251
Qy	316	SYNVIREDNNTNRLRSLLDFESIWNNRWLRTISILFLNKQDLMAEKVLGAKS	375
Db	252	SYNVIREDNQTNRLQALNLFKSIWNNRWLRTISVILFNKQDLMAEKVLGAKS	311
Qy	376	PPEYANTVPEDATPDAGEDPKVTRAKFFIRDLFLRISTATGDKGHYCVPH	435
Db	312	PPEFARTYTTEDATPEGEDPRVTRAKYFIRDEFRLISTASDGRHYCVPH	371
Qy	436	IRRVFNCRDIIQRMHLKQYELL 458	
Db	372	IRRVFNCRDIIQRMHLRQYELL 394	
RESULT 10			
RGHYA2			
GTP-binding regulatory protein Gs alpha-2 chain (adenylate cyclase-stimulating			
N;Alternate names: guanine nucleotide binding protein Gs alpha-2 chain; hetero			
C;Species: Mesocricetus auratus (golden hamster)			
C;Date: 31-Dec-1992 #sequence_revision 31-Dec-1992 #text_change 09-Jul-2004			
C;Accession: S10508			
R;Conner, D.A.; Feldman, A.M.; van Dop, C.			
Nucleic Acids Res. 18, 4279, 1990			
A;Title: cDNA sequence for the alpha subunit of the guanine nucleotide-binding			
A;Reference number: S10508; MUID: 90332451; PMID: 2115997			
A;Accession: S10508			
A;Molecule type: mRNA			
A;Residues: 1-394 <CON>			
A;Cross-references: UNIPROT:P04894; UNIPARC:UIPO000001ACB; EMBL:X53139; NID:G4			
C;Comment: The G proteins are a family of guanine nucleotide-binding proteins b			
ains. The beta and gamma chains, required for GTPase activity, appear to be con			
rase; it is specific for each type of G protein.			
C;Comment: The Gs alpha chain is specific for G protein that is responsible for			
rgic stimuli.			
C;Superfamily: GTP-binding regulatory protein Gs alpha chain			
C;Keywords: alternative splicing; blocked amino end; GTP binding; heterotrimer			
F;2-394/Product: GTP-binding regulatory protein Gs alpha-2 chain #status predi			
F;47-54/Region: nucleotide-binding motif A (P-loop)			
F;292-295/Region: GTP-binding NKXD motif			
F;2/Modified site: myristylated amino end (Gly) (in mature form) #status predi			
F;3/Binding site: palmitate (Cys) (covalent) #status predicted			
F;201/Modified site: ADP-ribosylarginine (Arg) (by cholera toxin) #status pred			
Query Match 63.4%; Score 1520.5; DB 1; Length 394;			
Best Local Similarity 73.4%; Pred. No. 1.1e-89;			
Matches 281; Conservative 45; Mismatches 42; Indels 15; Gaps 1			
Qy	91	EREAVTEARKVSRGIDRLMLDQKRDLOOQTHRLLLLGAGESGKSTIVKQMRILHVN	150
Db	12	QRNEEKAQREANKKIEKQLOKDQKVYRATHRLLLLGAGESGKSTIVKQMRILHVN	71
Qy	151	-----EKKQKILDIRKVNKDAIVTVISAMSTIIPVPLANPENQFRSDYI	195
Db	72	GGEEDPQAARNSDGEKATKVDQIKNNLKEAETIIVAAMSNLVPVELANPENQFRVDYI	131
Qy	196	KSIAPITDFBSYQBFDFHVKKLWDEGVKACFERSNEYQLIDCAQYFLERIDSV	255
Db	132	LSVMNVNFPDFPFYEYHAKALWDEGVACFERSNEYQLIDCAQYFLDKIDVI	191
Qy	256	PTDQLLRCRLVTSGIFETRFQVDKVNPFMDVGQDERRRKAQICFNDVTAIL	315
Db	192	PSDQLLRCRLVTSGIFETRFQVDKVNPFMDVGQDERRRKAQICFNDVTAIL	251
Qy	316	SYNVIREDNNTNRLRSLLDFESIWNNRWLRTISILFLNKQDLMAEKVLGAKS	375
Db	252	SYNVIREDNQTNRLQALNLFKSIWNNRWLRTISVILFNKQDLMAEKVLGAKS	311
Qy	376	PPEYANTVPEDATPDAGEDPKVTRAKFFIRDLFLRISTATGDKGHYCVPH	435
Db	312	PPEFARTYTTEDATPEGEDPRVTRAKYFIRDEFRLISTASDGRHYCVPH	371
Qy	436	IRRVFNCRDIIQRMHLKQYELL 458	
Db	372	IRRVFNCRDIIQRMHLRQYELL 394	
RESULT 10			
RGHYA2			
GTP-binding regulatory protein Gs alpha-2 chain (adenylate cyclase-stimulating			
N;Alternate names: guanine nucleotide binding protein Gs alpha-2 chain; hetero			
C;Species: Mesocricetus auratus (golden hamster)			
C;Date: 31-Dec-1992 #sequence_revision 31-Dec-1992 #text_change 09-Jul-2004			
C;Accession: S10508			
R;Conner, D.A.; Feldman, A.M.; van Dop, C.			
Nucleic Acids Res. 18, 4279, 1990			
A;Title: cDNA sequence for the alpha subunit of the guanine nucleotide-binding			
A;Reference number: S10508; MUID: 90332451; PMID: 2115997			
A;Accession: S10508			
A;Molecule type: mRNA			
A;Residues: 1-394 <CON>			
A;Cross-references: UNIPROT:P04894; UNIPARC:UIPO000001ACB; EMBL:X53139; NID:G4			
C;Comment: The G proteins are a family of guanine nucleotide-binding proteins b			
ains. The beta and gamma chains, required for GTPase activity, appear to be con			
rase; it is specific for each type of G protein.			
C;Comment: The Gs alpha chain is specific for G protein that is responsible for			
rgic stimuli.			
C;Superfamily: GTP-binding regulatory protein Gs alpha chain			
C;Keywords: alternative splicing; blocked amino end; GTP binding; heterotrimer			
F;2-394/Product: GTP-binding regulatory protein Gs alpha-2 chain #status predi			
F;47-54/Region: nucleotide-binding motif A (P-loop)			
F;292-295/Region: GTP-binding NKXD motif			
F;2/Modified site: myristylated amino end (Gly) (in mature form) #status predi			
F;3/Binding site: palmitate (Cys) (covalent) #status predicted			
F;201/Modified site: ADP-ribosylarginine (Arg) (by cholera toxin) #status pred			
Query Match 63.4%; Score 1520.5; DB 1; Length 394;			
Best Local Similarity 73.4%; Pred. No. 1.1e-89;			
Matches 281; Conservative 45; Mismatches 42; Indels 15; Gaps 1			

QY 256 PTQDILLRCRVLTSGIFETKFOVDKVNPHMFVGGQDERRKWIQCFNDVTAIIYVAACS 315
 Db 192 PSQDILLRCRVLTSGIFETKFOVDKVNPHMFVGGQDERRKWIQCFNDVTAIIYFVASS 251
 QY 316 SYNWVIREDNNTNRLRESLDLFPESIWNNRWLRTISIILFNKQDMLAEKVLAKSKIEDY 375
 Db 252 SYNWVIREDNQTNRLQEALNLFKSIWNNRWLRTISVILFNKQDMLAEKVLAKSKIEDY 311
 QY 376 PPEYANTVPEDATPDAGDPKVTYRAKFFIRDLPLRISTATGDKGHYCYPHFTCAVDTEN 435
 Db 312 PPEFARYTTPEDATPEGDPKVTYRAKFFIRDEFLRISTASGGRHYCYPHFTCAVDTEN 371
 QY 436 IRRVFNDCRDIQRMHLKQYELL 458
 Db 372 IRRVFNDCRDIQRMHLRQYELL 394

RESULT 11
 RGR7A2
 GTP-binding regulatory protein Gs alpha-2 chain (adenylate cyclase-stimulating) - rat
 N;Alternate names: guanine nucleotide binding protein Gs alpha-2 chain; heterotrimeric G
 C;Species: Rattus norvegicus (Norway rat)
 C;Date: 31-Dec-1992 #sequence_revision 31-Dec-1992 #text_change 09-Jul-2004
 C;Accession: A27423; C24882
 R;Jones, D.T.; Reed, R.R.
 J. Biol. Chem. 262, 14241-14249, 1987
 A;Title: Molecular cloning of five GTP-binding protein cDNA species from rat olfactory r
 A;Reference number: A92614; MUID:88007678; PMID:2820999
 A;Accession: A27423
 A;Molecule type: mRNA
 A;Residues: 1-394 <JON>
 A;Cross-references: UNIPROT:P04894; UNIPARC:UPI00000001ACB; GB:M17525; NID:g203171; PIDN:
 R;Itoh, H.; Kozasa, T.; Nagata, S.; Nakamura, S.; Katada, T.; Ui, M.; Iwai, S.; Ohseuka,
 Proc. Natl. Acad. Sci. U.S.A. 83, 3776-3780, 1986
 A;Title: Molecular cloning and sequence determination of cDNAs for alpha subunits of the
 A;Reference number: A94707; MUID:86233317; PMID:3086867
 A;Accession: C24882
 A;Molecule type: mRNA
 A;Residues: 1-394 <ITO>
 A;Cross-references: UNIPARC:UPI00000001ACB; GB:M12673; NID:g204441; PIDN:AAA41261.1; PID:
 C;Comment: The G proteins are a family of guanine nucleotide-binding proteins that relay
 ains. The beta and gamma chains, required for GTPase activity, appear to be common to al
 rase; it is specific for each type of G protein.
 C;Comment: The Gs alpha chain is specific for G protein that is responsible for transduc
 rgic stimuli.
 C;Superfamily: GTP-binding regulatory protein Gs alpha chain
 C;Keywords: blocked amino end; GTP binding; lipoprotein; myristylation; nucleotide bindi
 F;2-394/Product: GTP-binding regulatory protein Gs alpha-2 chain #status predicted <MAT>
 F;47-54/Region: nucleotide-binding motif A (P-loop)
 F;292-295/Region: GTP-binding NKXD motif
 F;2/Modified site: myristylated amino end (Gly) (in mature form) #status predicted
 F;3/Binding site: palmitate (Cys) (covalent) #status predicted
 F;201/Modified site: ADP-ribosylarginine (Arg) (by cholera toxin) #status predicted

Query Match 63.4%; Score 1520.5; DB 1; Length 394;
 Best Local Similarity 73.4%; Pred. No. 1.1e-89;
 Matches 281; Conservative 45; Mismatches 42; Indels 15; Gaps 1;

QY 91 EREAVKEARKVSRGIDRMRLDQKRDLOQTHRLLLLGAGESGKSTIVKQMRILHVGNGNPE 150
 Db 12 QRNEEKAQREANKKIEKQKQVYRATHRLLLLGAGESGKSTIVKQMRILHVGNGE 71

QY 151 EKKQKILDIRKNVKDAIVTIVSAMSTIIPVPLANPENQFRSDYIKSIAPITDFEYSQEF 210
 Db 72 EKATKQDQIKNNLKEAETIIVAAMSNLVPVELANPENQFRVDYILSVNVPDFDPPEF 131

QY 211 FPHVKLWDEGVKACFERSNEYQLIDCAQYFLERIDSVLDYDTDDOILLRCRVLTSG 270
 Db 132 YEHAHALWEDEGVACRYERSNEYQLIDCAQYFLDKIDVVKQDDYVPSDQILLRCRVLTSG 191

QY 271 IFETRFQVDKVNPHMFVGGQDERRKWIQCFNDVTAIIYVAACSNNVWVIREDNNTNRL 330
 Db 192 IFETRFQVDKVNPHMFVGGQDERRKWIQCFNDVTAIIYFVASSNNVWVIREDNQTNRL 251

QY 331 RESLDLFPESIWNNRWLRTISIILFNKQDMLAEKVLAKSK-----I 372
 Db 252 QEALNLFKSIWNNRWLRTISVILFNKQDMLAEKVLAKSKIELFVLDDRLRQERPF 311

QY 373 EYFFPYANTVPEDATPDAGDPKVTYRAKFFIRDLFLRISTATGDKGHYCYPHFTCAVD 432
 Db 312 EYFFPEFARYTTPEDATPEGDPKVTYRAKFFIRDEFLRISTASGGRHYCYPHFTCAVD 371

QY 433 TENIRRVFNDCRDIQRMHLKQYELL 458

Db 192 PSQDILLRCRVLTSGIFETKFOVDKVNPHMFVGGQDERRKWIQCFNDVTAIIYFVASS 251
 QY 316 SYNWVIREDNNTNRLRESLDLFPESIWNNRWLRTISIILFNKQDMLAEKVLAKSKIEDY 375
 Db 252 SYNWVIREDNQTNRLQEALNLFKSIWNNRWLRTISVILFNKQDMLAEKVLAKSKIEDY 311
 QY 376 PPEYANTVPEDATPDAGDPKVTYRAKFFIRDLPLRISTATGDKGHYCYPHFTCAVDTEN 435
 Db 312 PPEFARYTTPEDATPEGDPKVTYRAKFFIRDEFLRISTASGGRHYCYPHFTCAVDTEN 371
 QY 436 IRRVFNDCRDIQRMHLKQYELL 458
 Db 372 IRRVFNDCRDIQRMHLRQYELL 394

RESULT 12
 RGFCA2
 GTP-binding regulatory protein Gs alpha-2 chain (adenylate cyclase-stimulating) - pig
 N;Alternate names: guanine nucleotide binding protein Gs alpha-2 chain; heterotrimeric G
 C;Species: Sus scrofa domestica (domestic pig)
 C;Date: 31-Dec-1992 #sequence_revision 31-Dec-1992 #text_change 09-Jul-2004
 C;Accession: S18963
 R;Roth, D.A.; Kay, R.A.M.; Hammond, H.K.
 submitted to the EMBL Data Library, January 1992
 A;Reference number: S18963
 A;Accession: S18963
 A;Molecule type: mRNA
 A;Residues: 1-397 <ROT>
 A;Cross-references: UNIPROT:P29797; UNIPARC:UPI0000128208; EMBL:X63893; NID:g1957; PIDN:(
 C;Comment: The G proteins are a family of guanine nucleotide-binding proteins that relay
 ains. The beta and gamma chains, required for GTPase activity, appear to be common to al
 rase; it is specific for each type of G protein.
 C;Comment: The Gs alpha chain is specific for G protein that is responsible for transduc
 rgic stimuli.
 C;Superfamily: GTP-binding regulatory protein Gs alpha chain
 C;Keywords: alternative splicing; blocked amino end; GTP binding; heterotrimer; lipoprote
 F;2-397/Product: GTP-binding regulatory protein Gs alpha-2 chain #status predicted <MAT>
 F;47-54/Region: nucleotide-binding motif A (P-loop)
 F;277-280/Region: GTP-binding NKXD motif
 F;2/Modified site: myristylated amino end (Gly) (in mature form) #status predicted
 F;3/Binding site: palmitate (Cys) (covalent) #status predicted
 F;186/Modified site: ADP-ribosylarginine (Arg) (by cholera toxin) #status predicted

Query Match 63.2%; Score 1518; DB 1; Length 397;
 Best Local Similarity 72.8%; Pred. No. 1.7e-89;
 Matches 281; Conservative 45; Mismatches 42; Indels 18; Gaps 1;

QY 91 EREAVKEARKVSRGIDRMRLDQKRDLOQTHRLLLLGAGESGKSTIVKQMRILHVGNGNPE 150
 Db 12 QRNEEKAQREANKKIEKQKQVYRATHRLLLLGAGESGKSTIVKQMRILHVGNGD 71

QY 151 EKKQKILDIRKNVKDAIVTIVSAMSTIIPVPLANPENQFRSDYIKSIAPITDFEYSQEF 210
 Db 72 EKATKQDQIKNNLKEAETIIVAAMSNLVPVELANPENQFRVDYILSVNVPDFDPPEF 131

QY 211 FPHVKLWDEGVKACFERSNEYQLIDCAQYFLERIDSVLDYDTDDOILLRCRVLTSG 270
 Db 132 YEHAHALWEDEGVACRYERSNEYQLIDCAQYFLDKIDVVKQDDYVPSDQILLRCRVLTSG 191

QY 271 IFETRFQVDKVNPHMFVGGQDERRKWIQCFNDVTAIIYVAACSNNVWVIREDNNTNRL 330
 Db 192 IFETRFQVDKVNPHMFVGGQDERRKWIQCFNDVTAIIYFVASSNNVWVIREDNQTNRL 251

QY 331 RESLDLFPESIWNNRWLRTISIILFNKQDMLAEKVLAKSK-----I 372
 Db 252 QEALNLFKSIWNNRWLRTISVILFNKQDMLAEKVLAKSKIELFVLDDRLRQERPF 311

QY 373 EYFFPYANTVPEDATPDAGDPKVTYRAKFFIRDLFLRISTATGDKGHYCYPHFTCAVD 432
 Db 312 EYFFPEFARYTTPEDATPEGDPKVTYRAKFFIRDEFLRISTASGGRHYCYPHFTCAVD 371

QY 433 TENIRRVFNDCRDIQRMHLKQYELL 458

Db 372 TENIRRVFNDRCRIIORMHLRQYELL 397

RESULT 13

RBOGA

GTP-binding regulatory protein Gs alpha-2 chain (adenylate cyclase-stimulating) - bovine
N;Alternate names: guanine nucleotide binding protein Gs alpha-2 chain; heterotrimeric G
C;Species: Bos primigenius taurus (cattle)
C;Date: 28-Dec-1987 #sequence_revision 28-Dec-1987 #text_change 09-Jul-2004
C;Accession: A23818; A23615; A23813
R;Robshaw, J.D.; Russell, D.W.; Harris, B.A.; Smigel, M.D.; Gilman, A.G.
Proc. Natl. Acad. Sci. U.S.A. 83, 1251-1255, 1986
A;Title: Deduced primary structure of the alpha subunit of the GTP-binding stimulatory P
A;Reference number: A23813; MUID:86149283; PMID:3081893
A;Accession: A23818
A;Molecule type: mRNA
A;Residues: 1-394 <RBO>
A;Cross-references: UNIPROT:P04896; UNIPARC:UPI000016C31A; GB:M13006; NID:g161127; PIDN:
R;Nukada, T.; Tanabe, T.; Takahashi, H.; Noda, M.; Hirose, T.; Inayama, S.; Numa, S.
FEBS Lett. 195, 220-224, 1986
A;Title: Primary structure of the alpha-subunit of bovine adenylate cyclase-stimulating
A;Reference number: A23615; MUID:86108870; PMID:3080331
A;Accession: A23615
A;Molecule type: mRNA
A;Residues: 1-17, 'A', 19-84, 'D', 86-362, 'F', 364-394 <NUK>
A;Cross-references: UNIPARC:UPI000012B204; GB:M13006
C;Comment: The G proteins are a family of guanine nucleotide-binding proteins that relay
a signal. The beta and gamma chains, required for GTPase activity, appear to be common to all
types; it is specific for each type of G protein.
C;Comment: The Gs alpha chain is specific for G protein that is responsible for transduc
tion stimuli.

C;Superfamily: GTP-binding regulatory protein Gs alpha chain
C;Keywords: alternative splicing; blocked amino end; GTP binding; heterotrimer; lipoprot
F;2-394/Product: GTP-binding regulatory protein Gs alpha-2 chain #status predicted <MAT
F;47-54/Region: nucleotide-binding motif A (P-loop)
F;292-295/Region: GTP-binding NKXD motif
F;2/Modified site: myristylated amino end (Gly) (in mature form) #status predicted
F;3/Binding site: palmitate (Cys) (covalent) #status predicted
F;201/Modified site: ADP-ribosylarginine (Arg) (by cholera toxin) #status predicted

Query Match 63.18; Score 1513.5; DB 1; Length 394;
Best Local Similarity 73.48; Pred. No. 3.2e-89; Indels 15; Gaps 1;
Matches 281; Conservative 44; Mismatches 43

Qy 91 EBAVKEARKVSRGIDRMLDQKRDLOOQTHRLLLGAGESGKSTIVKQMLHVNQNP 150
Db 12 QRNEKGQREANKKIEKQKQKQVYRATHRLLLGAGESGKSTIVKQMLHVNQNP 71
Qy 151 -----EKKQKILDIRKNVKDAIVTIVSAMSTIIPVPLANPENQFRSDYI 195
Db 72 GGBEDPQARSNSGGERATKVQDIKNLKEAETIVAAMSNLVPVVELANPENQFRVDYI 131
Qy 196 KSTAPITDFEYSQEFFDHVKLWDEGVKACFERSNEYQLIDCAQYFLERIDSVSLVDYT 255
Db 132 LSNVNVDPDFPFPEFYEHAKALWEDEGVACYSERSNEYQLIDCAQYFLERIDSVSLVDYT 191
Qy 256 PTQDILRCRLVLTSGIFETRFQVDKVNFMFVGGQDERRKKTQCFNDVTIIVAAVS 315
Db 192 PSQDILRCRLVLTSGIFETRFQVDKVNFMFVGGQDERRKKTQCFNDVTIIVFASS 251
Qy 316 SYNVRDNNRLRESLDPESINWNRWLTISILFLNKQDLAEKVLGAKSKIEDY 375
Db 252 SYNVRDNNRLRESLDPESINWNRWLTISILFLNKQDLAEKVLGAKSKIEDY 311
Qy 376 FPEYANTVPEDATPDAGEPKVTRAKFFIRDLFLRISTATDGKHYCYPHFTCAVDTEN 435
Db 312 FPEYANTVPEDATPDAGEPKVTRAKFFIRDLFLRISTATDGKHYCYPHFTCAVDTEN 371
Qy 436 IRRVFNDCRDIIOHMLRQYELL 458
Db 372 IRRVFNDCRDIIOHMLRQYELL 394

RESULT 14

S34421

GTP-binding regulatory protein Gs alpha chain - human
C;Species: Homo sapiens (man)
C;Date: 08-Dec-1993 #sequence_revision 26-May-1995 #text_change 09-Jul-2004
C;Accession: S34421; S40964
R;Swaroop, A.; Agarwal, N.; Gruen, J.R.; Bick, D.; Weissman, S.M.
Nucleic Acids Res. 19, 4723-4729, 1991
A;Title: Differential expression of novel Gs-alpha signal transduction protein cDNA spec
A;Reference number: S34421; MUID:91367671; PMID:1716359
A;Accession: S34421
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: mRNA
A;Residues: 1-419 <SNA>
A;Cross-references: UNIPROT:Q14455; UNIPARC:UPI0000073FD3; EMBL:X56009; NID:g31916; PIDN:
R;Ali, I.U.; Reinhold, W.; Salvador, C.; Aguanno, S.
Nucleic Acids Res. 20, 4263-4267, 1992
A;Title: Aberrant splicing of Gs-alpha transcript in transformed human astroglial and gl
A;Reference number: S40964; MUID:92375734; PMID:1324476
A;Accession: S40964
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 112-116;236-242;263-264;268-275;279-286;306-309 <ALI>
A;Cross-references: UNIPARC:UPI000017513F; UNIPARC:UPI0000177863; UNIPARC:UPI0000177864;
C;Superfamily: GTP-binding regulatory protein Gs alpha chain

Query Match 60.88; Score 1460; DB 2; Length 419;
Best Local Similarity 63.48; Pred. No. 8.8e-86;
Matches 287; Conservative 41; Mismatches 71; Indels 54; Gaps 5;

Qy 26 PVEDAQPAPALAPVRAAARDTARTLLPRGGEG-----SPACARPKADPKKQRTEQ 80
Db 1 PVSSAPRRGHSA---SAPRSLQVAGRGGAALPCSLAPGCGAAGASPCP----- 50
Qy 81 LSAEERAAKERAARVAKRVSIGDIRMLDQKRDLOOQTHRLLLGAGESGKSTIVKQMR 140
Db 51 -GAGRRRAAGGRCCLACECTS-----LTCAGESGKSTIVKQMR 86
Qy 141 ILHVNQFNPE-----EKKQKILDIRKNVKDAIVTIVSAMSTIIPVPLAN 185
Db 87 ILHVNQFNQEGGEDPQARSNSDGERATKVQDIKNLKEAETIVAAMSNLVPVVELAN 146
Qy 186 PENQFRSDYIKSIAPITDFEYSQEFFDHVKLWDEGVKACFERSNEYQLIDCAQYFLER 245
Db 147 PENQFRVDYILSNVNVDPDFPFPEFYEHAKALWEDEGVACYSERSNEYQLIDCAQYFLDK 206
Qy 246 IDSVSLVDYTPDQDILRCRLVLTSGIFETRFQVDKVNFMFVGGQDERRKKTQCFNDV 305
Db 207 IDVIKQADYVPSDQDILRCRLVLTSGIFETRFQVDKVNFMFVGGQDERRKKTQCFNDV 266
Qy 306 TAIIVVAACSSYNMVRDNNRLRESLDPESINWNRWLTISILFLNKQDLAEKV 365
Db 267 TAIIVFASSYNMVRDNNRLRESLDPESINWNRWLTISILFLNKQDLAEKV 326
Qy 366 LAGSKIEDYFPEYANTVPEDATPDAGEPKVTRAKFFIRDLFLRISTATDGKHYCY 425
Db 327 LAGSKIEDYFPEYANTVPEDATPDAGEPKVTRAKFFIRDLFLRISTATDGKHYCY 386
Qy 426 HFTCAVDTENIRRVFNDCRDIIOHMLRQYELL 458
Db 387 HFTCAVDTENIRRVFNDCRDIIOHMLRQYELL 419

RESULT 15

S27015

GTP-binding regulatory protein Gs alpha chain - great pond snail
N;Alternate names: guanine nucleotide-binding protein Gs alpha-s chain
C;Species: Lymnaea stagnalis (great pond snail)
C;Date: 07-Apr-1994 #sequence_revision 07-Apr-1994 #text_change 09-Jul-2004
C;Accession: S27015; S25590
R;Knol, J.C.; Weidemann, W.; Planta, R.J.; Vreugdenhil, E.; van Heerikhuizen, H.
FEBS Lett. 314, 215-219, 1992

A:Title: Molecular cloning of G protein alpha subunits from the central nervous system c
A:Reference number: S27013; MUID:93106153; PMID:1468550
A:Accession: S27015
A:Molecule type: mRNA
A:Residues: 1-376 <KNO1>
A:Cross-references: UNIPROT:P30684; UNIPARC:UPI0000177868; EMBL:Z15096
R:Knol, J.C.; Weidemann, W.; Plantak, R.J.; Vreugdenhil, E.; van Heerikhuizen, H.
submitted to the EMBL Data Library, September 1992
A:Description: Molecular cloning of G protein alpha subunits that are expressed in the c
A:Reference number: S25598
A:Accession: S25590
A:Molecule type: mRNA
A:Residues: 1-64, 'F', '66-93, 'T', '95-358, 'D', '360-376 <KNO2>
A:Cross-references: UNIPARC:UPI0000128207; EMBL:Z15096; NID:99634; PIDN:CAA78808.1; PID:
C:Superfamily: GTP-binding regulatory protein Gs alpha chain
C:Keywords: GTP binding; nucleotide binding; P-loop; signal transduction
F:44-51/Region: nucleotide-binding motif A (P-loop)
F:274-277/Region: GTP-binding NKXD motif

Query Match	58.9%	Score	1413	DB 2	Length	376			
Best Local Similarity	71.0%	Pred. No.	7.7e-83						
Matches	262	Conservative	50	Mismatches	57	Indels	0	Gaps	0

Qy	90	KEREAVKEARKVSGIDRMLRQDKRDLQOTHRLLLLGAGESGKSTIVKOMRILHVGNP	149
Db	8	RDEDDKLRKEANKKIEQLAKDLLRYGTHRLLLLGAGESGKSTIVKOMRILHVNGLS	67
Qy	150	EEKQKILDIRKNVKDAIVTIVSAMSTIIPVPIANPENQFRSDYIKSIAPITDFEYSQE	209
Db	68	EERQKIEDIRKNVRDAITLTITGAMSNLNPVQLEHPONKAKVDYIQDKASQAEFDYPP	127
Qy	210	PFDAHVKKLWDGEGVKCAFERNEXQLIDCAQYFLERDSVLDVYPTPDOLLRCRVLT	269
Db	128	FYEITLWKDKGVQAFERNEXQLIDCAQYFDRVHIIRQAEYITSEQDILRCRVLT	187
Qy	270	GIFETRFQVDKNVFMFDVGQDERRRKWIOCFNDVTAIIVAAACSSYNNMVRDNNITNR	329
Db	188	GIPETKSVVDKNVFMFDVGQDERRRKWIOCFNDVTAIIVTACSGYNNVLREDATQNR	247
Qy	330	LRESLDLPESIVNNRWLRBTISIILFLNKQDMAEKVLGAKSKI EDPPEYANYTVPEDAT	389
Db	248	LKESLDLPFSIVNNRWLRBTISIVILFLNKQDLAEKVKAGSKI EDPPEYARYQVPDPAS	307
Qy	390	PDAGEDPKVTRAKFFIRDLFLRISTATGDGHXYCYPHETCAVDTENIRRVNDCRDIIR	449
Db	308	SEGEDTEVTRAKFFIRDEFRLRISTASDGRHYCYPHETCAVDTENIRRVNDCRDIIR	367
Qy	450	MHLKQYELL	458
Db	368	MHLRQYELL	376

Search completed: March 2, 2006, 19:31:05
Job time : 28.1616 secs

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: March 2, 2006, 19:29:50 ; Search time 286.601 Seconds
(without alignments)
1127.462 Million cell updates/sec

Title: US-10-618-320A-1

Perfect score: 2400

Sequence: 1 MGICYSLRPLIFGPGDDPC.....VFNDCRDIQRMHLKQYELL 458

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Uniprot 05.80.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	2400	100.0	458	Q86XU3_HUMAN	Q86XU3 homo sapien
2	2124	88.5	448	Q66147_MOUSE	Q66147 mus musculus
3	1847	77.0	351	Q8N2B4_HUMAN	Q8N2B4 homo sapien
4	1819	75.8	381	GNAL_HUMAN	P38405 homo sapien
5	1819	75.8	381	GNAL_MOUSE	Q8CCK7 mus musculus
6	1811	75.5	381	GNAL_RAT	P38406 rattus norv
7	1755	73.1	462	Q6GLL1_XENLA	Q6GLL1 xenopus lae
8	1677	69.9	379	Q90WN6_XENLA	Q90WN6 xenopus lae
9	1639	68.3	379	Q6PUS6_BRARE	Q6PUS6 brachydanio
10	1620	67.5	399	Q6DG15_BRARE	Q6DG15 brachydanio
11	1609	67.0	379	Q5U3H6_BRARE	Q5U3H6 brachydanio
12	1567.5	65.3	485	Q5FWY2_HUMAN	Q5FWY2 homo sapien
13	1563	65.1	722	Q5JWF1_HUMAN	Q5JWF1 homo sapien
14	1559	65.0	736	Q5JWF2_HUMAN	Q5JWF2 homo sapien
15	1559	65.0	756	Q9ZLN8_MOUSE	Q9ZLN8 mus musculus
16	1555	64.8	1133	Q6ROH7_MOUSE	Q6ROH7 mus musculus
17	1548	64.5	715	Q63803_RAT	Q63803 rattus norv
18	1540	64.2	379	Q6NXS0_HUMAN	Q6NXS0 homo sapien
19	1540	64.2	379	Q14433_HUMAN	Q14433 homo sapien
20	1529.5	63.7	380	Q5JWD2_HUMAN	Q5JWD2 homo sapien
21	1528	63.7	379	Q6P413_XENLA	Q6P413 xenopus lae
22	1527	63.6	379	GNAS_XENLA	P24799 xenopus lae
23	1525.5	63.6	394	GNAS_CANFA	P63091 canis famil
24	1525.5	63.6	394	GNAS_HUMAN	P63092 homo sapien
25	1525.5	63.6	394	Q5JWD5_HUMAN	Q5JWD5 homo sapien
26	1525	63.5	395	Q5JWD4_HUMAN	Q5JWD4 homo sapien
27	1522.5	63.4	394	GNAS_BOVIN	P04896 bos taurus
28	1521.5	63.4	394	GNAS_CRIGR	Q8R4A8 cricetus
29	1520.5	63.4	394	GNAS_CRILLO	P16052 cricetus
30	1520.5	63.4	394	GNAS_MESAU	P63093 mesocricetu
31	1520.5	63.4	394	GNAS_MOUSE	P63094 mus musculus

32	1520.5	63.4	394	1	GNAS_RAT	P63095 rattus norv
33	1520.5	63.4	394	2	Q58B62_MOUSE	Q58B62 mus musculus
34	1519	63.3	379	1	Q6NVN4_XENTR	Q6NVN4 xenopus tro
35	1518	63.2	397	1	GNAS_PIG	P29797 sus scrofa
36	1507	62.8	342	2	Q8TBC0_HUMAN	Q8TBC0 homo sapien
37	1495	62.3	340	2	Q6X973_RABIT	Q6X973 oryctolagus
38	1471	61.3	379	2	Q6QM14_LYTVA	Q6QM14 lytechinus
39	1463	61.0	379	2	Q6QM15_STRPU	Q6QM15 strongyloce
40	1462.5	60.9	379	1	GNAS_HOMAN	Q16118 homarus ame
41	1460	60.8	419	2	Q14455_HUMAN	Q14455 homo sapien
42	1458.5	60.8	362	2	Q9Z1R8_RAT	Q9Z1R8 rattus norv
43	1457.5	60.7	362	2	Q921R7_MOUSE	Q921R7 mus musculus
44	1457.5	60.7	417	2	Q5JWC5_HUMAN	Q5JWC5 homo sapien
45	1440.5	60.0	379	2	Q66Q60_PENVA	Q66Q60 penaeus van

ALIGNMENTS

RESULT 1

ID	Q86XU3_HUMAN PRELIMINARY;	PRT;	458 AA.
AC	Q86XU3;		
DT	01-JUN-2003 (TrEMBLrel. 24, Created)		
DT	01-JUN-2003 (TrEMBLrel. 24, Last sequence update)		
DT	01-MAR-2004 (TrEMBLrel. 26, Last annotation update)		
DE	Guanine nucleotide binding protein (G protein), alpha activating		
DE	activity polypeptide, olfactory type, isoform 1.		
GN	Names=GNAL;		
OS	Homo sapiens (Human)		
OC	Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Theria; Euarchontoglires; Primates; Catarrhini; Hominidae;		
OC	Homo.		
OX	NCBI_TaxID=9606;		
RN	[1]_TaxID=9606;		
RP	NUCLEOTIDE SEQUENCE.		
RC	TISSUE=Testis;		
RX	MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;		
RA	Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,		
RA	Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,		
RA	Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,		
RA	Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,		
RA	Brownstein M.J., Udell T.B., Toshyuki S., Carninci P., Prange C.,		
RA	Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,		
RA	Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,		
RA	Richards S., Muzny K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,		
RA	Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,		
RA	Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,		
RA	Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,		
RA	Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,		
RA	Butterfield J.S.N., Krzywinski M.I., Skalska U., Smallos D.E.,		
RA	Schmurch A., Schein J.E., Jones S.J.M., Marra M.A.,		
RT	"Generation and initial analysis of more than 15,000 full-length human		
RT	and mouse cDNA sequences."		
RL	Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).		
RN	[2]		
RP	NUCLEOTIDE SEQUENCE.		
RC	TISSUE=Testis;		
RG	NIH MGC Project;		
RL	Submitted (APR-2003) to the EMBL/GenBank/DBJ databases.		
DR	EMBL; BC050021; AH50021.1; -; mRNA.		
DR	HSSP; P04896; 1CJU.		
DR	SMR; Q86XU3; 117-455.		
DR	Ensembl; ENSG0000141404; Homo sapiens.		
DR	GO; GO:0005525; F-GTP binding; IEA.		
DR	GO; GO:0004871; F-signal transducer activity; IEA.		
DR	GO; GO:0007186; P-G-protein coupled receptor protein signalin. . .; IEA.		
DR	GO; GO:0007165; P-signal transduction; IEA.		
DR	InterPro; IPR001019; Gprotein_alpha_bd.		
DR	InterPro; IPR000367; Gprotein_alpha_S.		

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DR InterPro; IPR011025; Gproteina_insert.
DR Pfam; PF00503; G-alpha; 1.
DR PRINTS; PR00318; GPROTEINA.
DR PRINTS; PR00443; GPROTEINAS.
DR PRODOM; PD000281; Gproteina_alpha; 1.
DR SMART; SM00275; G_alpha; 1.
SQ SEQUENCE 458 AA; 52455 MW; 89231879924C06A1 CRC64;

Query Match 100.0%; Score 2400; DB 2; Length 458;
Best Local Similarity 100.0%; Pred. No. 7.9e-135;
Matches 458; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGLCYSLRPLFLFGPGDDPCAASEPPVEDAQAPAPALAPVRAAARDTARTLLPRGEGS 60
DB 1 MGLCYSLRPLFLFGPGDDPCAASEPPVEDAQAPAPALAPVRAAARDTARTLLPRGEGS 60
QY 61 PACARPKADPKPKRQRTQOLSABERAAKREAVKARVSRGIDRMRLDRQKRDLDQO 120
DB 61 PACARPKADPKPKRQRTQOLSABERAAKREAVKARVSRGIDRMRLDRQKRDLDQO 120
QY 121 RLLLLGAGESGKSTIVKQMRILHVGNFNPBEKKQKILDIRKNVKDAIVTIVSAMSTI 180
DB 121 RLLLLGAGESGKSTIVKQMRILHVGNFNPBEKKQKILDIRKNVKDAIVTIVSAMSTI 180
QY 181 VPLANPENQFRSDYIKSIAPITDFEYSQEFDFHVKLWDDGVKACFERSNEYQLIDCAQ 240
DB 181 VPLANPENQFRSDYIKSIAPITDFEYSQEFDFHVKLWDDGVKACFERSNEYQLIDCAQ 240
QY 241 YFLERIDSVSLVDYPTPDQDLRCRVLTSGIFETRFQVDKVNFMFVGVGQDRERKWIQ 300
DB 241 YFLERIDSVSLVDYPTPDQDLRCRVLTSGIFETRFQVDKVNFMFVGVGQDRERKWIQ 300
QY 301 CFNDVTAIIVAACSSYNMVIREDNNTNRLRESLDLFESEIWNRLRTISILFLNKQDM 360
DB 301 CFNDVTAIIVAACSSYNMVIREDNNTNRLRESLDLFESEIWNRLRTISILFLNKQDM 360
QY 361 LAEVLGAGSKIEDYFPEYANYTVPEDATPDAGEDPKVTRAKFFIRDLFLRISTATGDGK 420
DB 361 LAEVLGAGSKIEDYFPEYANYTVPEDATPDAGEDPKVTRAKFFIRDLFLRISTATGDGK 420
QY 421 HCYCPHPTCAVDTENIRRVNDCRDIIRMHKQYELL 458
DB 421 HCYCPHPTCAVDTENIRRVNDCRDIIRMHKQYELL 458

RESULT 2
Q66L47_MOUSE PRELIMINARY; PRT; 448 AA.
AC Q66L47;
DT 25-OCT-2004 (T-EMBLrel. 28, Created)
DT 25-OCT-2004 (T-EMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (T-EMBLrel. 28, Last annotation update)
DE Gnal protein.
GN Name=Gnal;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridea; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6; TISSUE=Brain;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strauberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udén T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McSwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
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RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalek U., Smailus D.E.,
RA Schnorch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6; TISSUE=Brain;
RG NIH MGC project;
RL Submitted (JUL-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC078439; AAH78439.1; -; mRNA.
DR SMR; Q66L47; 107-445.
DR Ensembl; ENSMUSG0000024524; Mus musculus.
DR MGI; MGI:95774; Gnal.
DR GO; GO:0007190; P:adenylate cyclase activation; IDA.
DR GO; GO:0007608; P:perception of smell; IMP.
DR InterPro; IPR001019; Gproteina_alpha_bd.
DR InterPro; IPR000367; Gproteina_alpha_S.
DR InterPro; IPR011025; Gproteina_insert.
DR Pfam; PF00503; G-alpha; 1.
DR PRINTS; PR00318; GPROTEINA.
DR PRINTS; PR00443; GPROTEINAS.
DR PRODOM; PD000281; Gproteina_alpha; 1.
DR SMART; SM00275; G_alpha; 1.
SQ SEQUENCE 448 AA; 51357 MW; AE192038B7E3B40E CRC64;

Query Match 88.5%; Score 2124; DB 2; Length 448;
Best Local Similarity 91.0%; Pred. No. 2.1e-118;
Matches 417; Conservative 6; Mismatches 25; Indels 10; Gaps 3;

QY 1 MGLCYSLRPLFLFGPGDDPCAASEPPVEDAQAPAPALAPVRAAARDTARTLLPRGEGS 60
DB 1 MGLCYSLRPLFLFGSPEDTCAASEPCAEDAQAPAPASIPAPA--PVGTLRRGGRI 58
QY 61 PACARPKADPKPKRQRTQOLSABERAAKREAVKARVSRGIDRMRLDRQKRDLDQO 120
DB 59 VANARPPGE--LQSRRRQQLRAEEREA-----KEARKVSRGIDRMRLREQKRDLDQO 110
QY 121 RLLLLGAGESGKSTIVKQMRILHVGNFNPBEKKQKILDIRKNVKDAIVTIVSAMSTI 180
DB 111 RLLLLGAGESGKSTIVKQMRILHVGNFNPBEKKQKILDIRKNVKDAIVTIVSAMSTI 170
QY 181 VPLANPENQFRSDYIKSIAPITDFEYSQEFDFHVKLWDDGVKACFERSNEYQLIDCAQ 240
DB 171 VPLANPENQFRSDYIKSIAPITDFEYSQEFDFHVKLWDDGVKACFERSNEYQLIDCAQ 230
QY 241 YFLERIDSVSLVDYPTPDQDLRCRVLTSGIFETRFQVDKVNFMFVGVGQDRERKWIQ 300
DB 231 YFLERIDSVSLVDYPTPDQDLRCRVLTSGIFETRFQVDKVNFMFVGVGQDRERKWIQ 290
QY 301 CFNDVTAIIVAACSSYNMVIREDNNTNRLRESLDLFESEIWNRLRTISILFLNKQDM 360
DB 291 CFNDVTAIIVAACSSYNMVIREDNNTNRLRESLDLFESEIWNRLRTISILFLNKQDM 350
QY 361 LAEVLGAGSKIEDYFPEYANYTVPEDATPDAGEDPKVTRAKFFIRDLFLRISTATGDGK 420
DB 351 LAEVLGAGSKIEDYFPEYANYTVPEDATPDAGEDPKVTRAKFFIRDLFLRISTATGDGK 410
QY 421 HCYCPHPTCAVDTENIRRVNDCRDIIRMHKQYELL 458
DB 411 HCYCPHPTCAVDTENIRRVNDCRDIIRMHKQYELL 448

RESULT 3
Q8N2B4_HUMAN
ID Q8N2B4_HUMAN PRELIMINARY; PRT; 351 AA.
AC Q8N2B4;
DT 01-OCT-2002 (T-EMBLrel. 22, Created)
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DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE Hypothetical protein FLJ33549.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
 OC Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Amrygdala;
 RX PubMed=14702039; DOI=10.1038/ng1285;
 RA Oka T., Suzuki Y., Nishikawa T., Otsuki T., Sugiyama T., Irie R.,
 RA Wakamatsu A., Hayaishi K., Sato H., Nagai K., Kimura K., Makita H.,
 RA Sekine M., Obayashi M., Nishi T., Shibahara T., Tanaka T., Ishii S.,
 RA Yamamoto J.-I., Saito K., Kawai Y., Isono Y., Nakamura Y.,
 RA Nagahara K., Murakami K., Yasuda T., Iwayanagi T., Wagatsuma M.,
 RA Shiratori A., Sudo H., Hosoiri T., Kaku Y., Kodaira H., Kondo H.,
 RA Sugawara M., Takahashi M., Kanda K., Yokoi T., Furuya T., Kikkawa E.,
 RA Omura Y., Abe K., Kamihara K., Katsuta N., Sato K., Tanikawa M.,
 RA Yamazaki M., Ninomiya K., Ishibashi T., Yamashita H., Murakawa K.,
 RA Fujimori K., Tanai H., Kimata M., Watanabe M., Hiraoka S., Chiba Y.,
 RA Ishida S., Ono Y., Takiguchi S., Watanabe S., Yoshida M., Hotuta T.,
 RA Kusano J., Kanehori K., Takahashi-Fujii A., Hara H., Tanase T.-O.,
 RA Nomura Y., Togiya S., Komai F., Hara R., Takeuchi K., Arita M.,
 RA Inose N., Musashino K., Yuuki H., Oshima A., Sasaki N., Aotsuka S.,
 RA Ioshikawa Y., Matsunawa H., Ichihara T., Shiohata N., Sano S.,
 RA Moriya S., Momiyama H., Satoh N., Takami S., Terashima Y., Suzuki O.,
 RA Nakagawa S., Senoh A., Mizoguchi H., Goto Y., Shimizu F., Wakebe H.,
 RA Hishigaki H., Watanabe T., Sugiyama A., Takemoto M., Kawakami B.,
 RA Yamazaki M., Watanabe K., Kunagai A., Itakura S., Fukuzumi Y.,
 RA Fujimori Y., Komiyama M., Tashiro H., Tanigami A., Fujiwara T.,
 RA Ono T., Yamada K., Fujii Y., Ozaki K., Hirao M., Ohmori Y.,
 RA Kawabata A., Hikiji T., Kobatake N., Inagaki H., Ikema Y., Okamoto S.,
 RA Kitatani R., Kawakami T., Noguchi S., Itoh T., Shigeta K., Senba T.,
 RA Matsumura K., Nakajima Y., Mizuno T., Morinaga M., Sasaki M.,
 RA Togaishi T., Oyama M., Hata H., Watanabe M., Komatsu T.,
 RA Mizushima-Sugano J., Satoh T., Shirai Y., Takahashi Y., Nakagawa K.,
 RA Okumura K., Nagase T., Nomura N., Kikuchi H., Masuho Y., Yamashita R.,
 RA Nakai K., Yada T., Nakamura Y., Ohara O., Isogai T., Sugano S.;
 RT "Complete sequencing and characterization of 21,243 full-length human
 RT cDNAs.";
 RL Nat. Genet. 36:40-45 (2004).
 DR EMBL; AK090868; BAC03535.1; --; mRNA.
 DR HSP; P04896; 1CJU.
 DR SMR; Q8N2B4; 10-348.
 DR GO; GO:0005525; F:GTP binding; IEA.
 DR GO; GO:0004871; F:signal transducer activity; IEA.
 DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. .; IEA.
 DR GO; GO:0007165; P:signal transduction; IEA.
 DR InterPro; IPR011025; Gprotein_alpha_insert.
 DR InterPro; IPR011019; Gprotein_alpha.
 DR InterPro; IPR003367; Gprotein_alpha_S.
 DR Pfam; PF00503; G-alpha; 1.
 DR PRINTS; PR03118; GPROTEIN.
 DR PRINTS; PR00443; GPROTEINAS.
 DR ProDom; PD000281; Gprotein_alpha; 1.
 DR SMART; SM00275; G_alpha; 1.
 SQ SEQUENCE 351 AA; 41057 MW; 4956B9D7573F9F60 CRC64;
 Query Match 77.0%; Score 1847; DB 2; Length 351;
 Best Local Similarity 100.0%; Pred. No. 4.9e-102;
 Matches 351; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 108 MLRDKEDLQTHRLLLGAGESGKSTIVKQMRILVHNGSPNPEKKQILDIRNKVDAL 167
 DB 1 MLRDKEDLQTHRLLLGAGESGKSTIVKQMRILVHNGSPNPEKKQILDIRNKVDAL 60
 QY 168 VTVSAMSTIIPVPLANPENQFRSDYIKSIAPITDPEYSQEFDFHVKLWDDEGVKACF 227
 DB 61 VTVSAMSTIIPVPLANPENQFRSDYIKSIAPITDPEYSQEFDFHVKLWDDEGVKACF 120
 QY 228 ERNEVQLIDCAQYFLERIDSVLVDYPTDQDLLRCRVLTSIGIFETRFQVDKVNFMFD 287

DB 121 ERNEVQLIDCAQYFLERIDSVLVDYPTDQDLLRCRVLTSIGIFETRFQVDKVNFMFD 180
 QY 288 VGGQDERRKWIQCFNDVTATIIYVAACSSNMVIRENNTNRLRESLDLFESIWNNWLR 347
 DB 181 VGGQDERRKWIQCFNDVTATIIYVAACSSNMVIRENNTNRLRESLDLFESIWNNWLR 240
 QY 348 TISIIILFLNKQDMLAEKVLGKSKIEDYFPEYANYTVPEDATPDAGDPPKTRAKFIRD 407
 DB 241 TISIIILFLNKQDMLAEKVLGKSKIEDYFPEYANYTVPEDATPDAGDPPKTRAKFIRD 300
 QY 408 LFLRISTATGDGHYCPHFTCAVDENIRRVFNDCKDIIQRMHLKQYELL 458
 DB 301 LFLRISTATGDGHYCPHFTCAVDENIRRVFNDCKDIIQRMHLKQYELL 351

RESULT 4
 ID GNAL HUMAN STANDARD; PRT; 381 AA.
 AC P38405;
 DT 01-OCT-1994 (Rel. 30, Created)
 DT 01-OCT-1994 (Rel. 30, Last sequence update)
 DT 13-SEP-2005 (Rel. 48, Last annotation update)
 DE Guanine nucleotide-binding protein G(olf), alpha subunit (Adenylate
 DE cyclase-stimulating G alpha protein, olfactory type).
 DE Name=GNAL;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
 OC Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Insulinoma;
 RX MEDLINE=94062616; PubMed=8243272; DOI=10.1210/en.133.6.2508;
 RA Zigman J.M.; Westmark G.T.; Lamendola J.; Boel E.; Steiner D.F.;
 RT "Human G(olf) alpha: complementary deoxyribonucleic acid structure and
 RT expression in pancreatic islets and other tissues outside the
 RT olfactory neuroepithelium and central nervous system.";
 RL Endocrinology 133:2508-2514 (1993).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RA Vuorio J.T., Berrettini W.H., Overhauser J., Prockop D.J.,
 RA Ferraro T.N., Ala-Kokko L.;
 RT "The gene for the human G protein Golf alpha.";
 RL Submitted (APR-1996) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
 RC TISSUE=Brain;
 RA Puhl H.L. III, Ikeda S.R., Aronstam R.S.;
 RT "cDNA clones of human proteins involved in signal transduction
 RT sequenced by the Guthrie cDNA resource center (www.cdna.org).";
 RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: Guanine nucleotide-binding proteins (G proteins) are
 CC involved as modulators or transducers in various transmembrane
 CC signaling systems. G(olf) alpha mediates signal transduction
 CC within the olfactory neuroepithelium and the basal ganglia. May be
 CC involved in some aspect of visual transduction, and in mediating
 CC the effect of one or more hormones/neurotransmitters.
 CC -1- SUBUNIT: G proteins are composed of 3 units; alpha, beta and
 CC gamma. The alpha chain contains the guanine nucleotide binding
 CC site.
 CC -1- TISSUE SPECIFICITY: Detected in olfactory neuroepithelium, brain,
 CC testis, and to a lower extent in retina, lung alveoli, spleen.
 CC Trace amounts where seen in kidney, adrenal gland and liver. Found
 CC to be expressed in all the insulinomas examined.
 CC -1- SIMILARITY: Belongs to the G-alpha family. G(s) subfamily.
 CC -----
 CC This Swiss-Prot entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use as long as its content is in no way modified and this statement is not
 CC removed.

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CC -----
DR EMBL; L10665; AAC37535.1; -; mRNA.
DR EMBL; U55184; AAD00085.1; -; Genomic DNA.
DR EMBL; U55180; AAD00085.1; JOINED; Genomic DNA.
DR EMBL; U55181; AAD00085.1; JOINED; Genomic DNA.
DR EMBL; U55182; AAD00085.1; JOINED; Genomic DNA.
DR EMBL; U55183; AAD00085.1; JOINED; Genomic DNA.
DR EMBL; AF493893; AAM12607.1; -; mRNA.
DR PIR; I53271; I53271.
DR HSSP; P04896; 1CJU.
DR SMR; P38405; 39-378.
DR ENSEMBL; ENSG0000041404; Homo sapiens.
DR HGNC; HGNC:4388; GNAL.
DR MIM; 139312; -.
DR GO; GO:0003924; P:GTPase activity; TAS.
DR GO; GO:0007165; P:signal transduction; TAS.
DR InterPro; IPR001019; Gprotein_alpha_bd.
DR InterPro; IPR000367; Gprotein_alpha_S.
DR InterPro; IPR011025; GproteinA_insert.
DR Pfam; PF00503; G-alpha; 1.
DR PRINTS; PR00318; GPROTEINA.
DR PRINTS; PR00443; GPROTEINAS.
DR ProDom; PD000281; Gprotein_alpha; 1.
KW ADP-ribosylation; GTP-binding; Lipoprotein; Multigene family;
KW Nucleotide-binding; Palmitate; Transducer.
FT NP_BIND 49 56 GTP (By similarity).
FT NP_BIND 210 214 GTP (By similarity).
FT NP_BIND 279 282 GTP (By similarity).
FT MOD_RES 188 188 ADP-ribosylarginine (by cholera toxin).
FT LIPID 3 3 S-palmitoyl cysteine (By similarity).
SQ SEQUENCE 381 AA; 44308 MW; 9A73D2982FF9CA3 CRC64;

Query Match 75.8%; Score 1819; DB 1; Length 381;
Best Local Similarity 95.0%; Pred. No. 2.5e-100;
Matches 345; Conservative 9; Mismatches 9; Indels 0; Gaps 0;

Qy 96 KEARKVSRGIDRLMDQKRLQDQLQTHRLLLGAGESGKSTIVKQWILHVNFGFPEKKQK 155
Db 19 KERREANKKIEKQLQKERLAYKATHRLLLGAGESGKSTIVKQWILHVNFGFPEKKQK 78

Qy 156 ILDIRKNVDAIVTVSAMSTIIPVPLANPENQFRSDYIKSIAPITDFEYSQEFDFHVK 215
Db 79 ILDIRKNVDAIVTVSAMSTIIPVPLANPENQFRSDYIKSIAPITDFEYSQEFDFHVK 138

Qy 216 KLWDDGVKACFRSEYQLIDCAQYELERIDSLSLVVDVYPTDQDLLRCRVLTSGIFETR 275
Db 139 KLWDDGVKACFRSEYQLIDCAQYELERIDSLSLVVDVYPTDQDLLRCRVLTSGIFETR 198

Qy 276 FOVDKVNFMFVGGQDERRKWTQCFNDVTAIYVAACSSYNVWIREDDNNTNRLRESLD 335
Db 199 FOVDKVNFMFVGGQDERRKWTQCFNDVTAIYVAACSSYNVWIREDDNNTNRLRESLD 258

Qy 336 LFESIMNRLWRTISILFLNKQDMLAEKVLACKSKIEDYFPEYANYVPEDATPDAGED 395
Db 259 LFESIMNRLWRTISILFLNKQDMLAEKVLACKSKIEDYFPEYANYVPEDATPDAGED 318

Qy 396 PKYTRAKFFRDILRISTATGDKHKYCYPHFTCAVDTENIRRVFNDRCRDIIRQMLKQY 455
Db 319 PKYTRAKFFRDILRISTATGDKHKYCYPHFTCAVDTENIRRVFNDRCRDIIRQMLKQY 378

Qy 456 ELL 458
Db 379 ELL 381

RESULT 5
ID GNAL_MOUSE STANDARD; PRT; 381 AA.
AC QRCGK7; Q61020; Q61589;
DT 29-MAR-2004 (Rel. 43, Created)
DT 29-MAR-2004 (Rel. 43, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Guanine nucleotide-binding protein G(olf), alpha subunit (Adenylate
cyclase-stimulating G alpha protein, olfactory type).
Name=Gnal;
Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
Muridae; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
[1]
RN NUCLEOTIDE SEQUENCE.
STRAIN=C57BL/6;
Von Dannecker L.E.C., Malnic B.;
"The mouse G protein Golf alpha subunit full length coding sequence.";
Submitted (NOV-2002) to the EMBL/GenBank/DBJ databases.
[2]
RN NUCLEOTIDE SEQUENCE OF 209-373.
STRAIN=CF-1 / Harlan; TISSUE=Brain;
MEDLINE=97011591; PubMed=8858601;
DOI=10.1002/(SICI)1098-2795(199607)44:3<315::AID-MRDS3.3.CO;2-V;
Williams C.J., Schultz R.M., Kopf G.S.;
"G protein gene expression during mouse oocyte growth and maturation,
and preimplantation embryo development.";
Mol. Reprod. Dev. 44:315-323(1996).
[3]
RN NUCLEOTIDE SEQUENCE OF 216-276.
TISSUE=Brain;
MEDLINE=90017488; PubMed=2508088;
Strathmann M., Wilkie T.M., Simon M.I.;
"Diversity of the G-protein family: sequences from five additional
alpha subunits in the mouse.";
Proc. Natl. Acad. Sci. U.S.A. 86:7407-7409(1989).
-!- FUNCTION: Guanine nucleotide-binding proteins (G proteins) are
involved as modulators or transducers in various transmembrane
signaling systems. G(olf) alpha mediates signal transduction
within the olfactory neuroepithelium and the basal ganglia. May be
involved in some aspect of visual transduction, and in mediating
the effect of one or more hormones/neurotransmitters (By
similarity).
-!- SUBUNIT: G proteins are composed of 3 units; alpha, beta and
gamma. The alpha chain contains the guanine nucleotide binding
site.
-!- SIMILARITY: Belongs to the G-alpha family. G(s) subfamily.
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between the Swiss Institute of Bioinformatics and the EMBL Outstation -
the European Bioinformatics Institute. There are no restrictions on its
use as long as its content is in no way modified and this statement is not
removed.
EMBL; AV179169; AAC03564.1; -; mRNA.
EMBL; U38503; AAB01734.1; -; mRNA.
EMBL; M57635; AAG63300.1; -; mRNA.
HSSP; P04896; 1CJU.
SMR; QRCGK7; 39-378.
Ensembl; ENSMUSG00000024524; Mus musculus.
MGI; MGI:95774; Gnal.
GO; GO:0007190; P:adenylate cyclase activation; IDA.
GO; GO:0007608; P:perception of smell; IMP.
InterPro; IPR001019; Gprotein_alpha_bd.
InterPro; IPR000367; Gprotein_alpha_S.
InterPro; IPR011025; GproteinA_insert.
Pfam; PF00503; G-alpha; 1.
PRINTS; PR00318; GPROTEINA.
PRINTS; PR00443; GPROTEINAS.
ProDom; PD000281; Gprotein_alpha; 1.
SMART; SM00275; G_alpha; 1.
KW ADP-ribosylation; GTP-binding; Lipoprotein; Multigene family;
KW Nucleotide-binding; Palmitate; Transducer.
FT NP_BIND 49 56 GTP (By similarity).
FT NP_BIND 210 214 GTP (By similarity).
FT NP_BIND 279 282 GTP (By similarity).
FT MOD_RES 188 188 ADP-ribosylarginine (by cholera toxin).
FT LIPID 3 3 S-palmitoyl cysteine (By similarity).

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SQ SEQUENCE 381 AA; 44308 MW; F707E668EC279033 CRC64;
Query Match 75.8%; Score 1819; DB 1; Length 381;
Best Local Similarity 95.0%; Pred. No. 2.5e-100;
Matches 345; Conservative 9; Mismatches 9; Indels 0; Gaps 0;

QY 96 KEARKVSRGIDRLMDQKRLDQOQTHRLLLGAGESGKSTIVKQMRILHVNPNPEKKQK 155
Db 19 KERREANKKLEKQKQERLAYKATHRLLLGAGESGKSTIVKQMRILHVNPNPEKKQK 78

QY 156 ILDIRKNVKDAIVTVISAMSTIIPPPVPLANPENQFRSDYIKSIAPITDFEYSOEFFDHVK 215
Db 79 ILDIRKNVKDAIVTVISAMSTIIPPPVPLANPENQFRSDYIKSIAPITDFEYSOEFFDHVK 138

QY 216 KLWDEGVKACFERSNEYQLIDCAQYFLERIDSLSVLDVYPTDQDLLRCRVLTSIGIFETR 275
Db 139 KLWDEGVKACFERSNEYQLIDCAQYFLERIDSLSVLDVYPTDQDLLRCRVLTSIGIFETR 198

QY 276 FQVDKYNFHMFDVGGQDERRKWIQCFNDVTAIYVAACSSYNMVIREDNNTNRLRESLD 335
Db 199 FQVDKYNFHMFDVGGQDERRKWIQCFNDVTAIYVAACSSYNMVIREDNNTNRLRESLD 258

QY 336 LFESIWNRLRTISILFLNKQDMLAEKVLACKSKIEDYFFPEYANTVPEDATPDAGED 395
Db 259 LFESIWNRLRTISILFLNKQDMLAEKVLACKSKIEDYFFPEYANTVPEDATPDAGED 318

QY 396 PKVTRAKFFIRDLFLRISTATGDKHYCPHFTCAVDTENIRRVFNDCRDIIQRMHLKQY 455
Db 319 PKVTRAKFFIRDLFLRISTATGDKHYCPHFTCAVDTENIRRVFNDCRDIIQRMHLKQY 378

QY 456 ELL 458
Db 379 ELL 381

RESULT 6
GNAL_RAT STANDARD; PRT; 381 AA.
ID GNAL_RAT
AC P38406; Q64711;
DT 01-OCT-1994 (Rel. 30, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Guanine nucleotide-binding protein G(olf), alpha subunit (Adenylate
DE cyclase-stimulating G alpha protein, olfactory type).
GN Names=Gnal;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutharia; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=89266882; PubMed=2495043;
RA Jones D.T., Reed R.R.;
RT "Golf: an olfactory neuron specific-G protein involved in odorant
RT signal transduction.";
RL Science 244:790-795(1989).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Sprague-Dawley; TISSUE=Brain;
RX MEDLINE=96115117; PubMed=7494450; DOI=10.1016/0169-328X(95)00070-9;
RA Herve D., Rogard M., Levi-Strauss M.;
RT "Molecular analysis of the multiple Golf alpha subunit mRNAs in the
RT rat brain.";
RL Brain Res. Mol. Brain Res. 32:125-134(1995).
CC -1- FUNCTION: Guanine nucleotide-binding proteins (G proteins) are
CC involved as modulators or transducers in various transmembrane
CC signaling systems. G(olf) alpha mediates signal transduction
CC within the olfactory neuroepithelium and the basal ganglia. May be
CC involved in some aspect of visual transduction, and in mediating
CC the effect of one or more hormones/neurotransmitters.
CC -1- SUBUNIT: G proteins are composed of 3 units; alpha, beta and
CC gamma. The alpha chain contains the guanine nucleotide binding

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RESULT 7
Q6GLL1_XENLA

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CC site.
CC -1- SIMILARITY: Belongs to the G-alpha family. G(s) subfamily.
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
CC ENBL; M26718; -; NOT_ANNOTATED_CDS; Unassigned_DNA.
CC ENBL; S80376; AAP32223.1; -; mRNA.
CC ENBL; S80330; -; NOT_ANNOTATED_CDS; mRNA.
CC HSSP; P04896; 1CJU.
CC SMR; P38406; 39-380.
CC Ensemble; ENSRNOG00000010440; Rattus norvegicus.
CC RGD; 2715; Gnal.
CC GO; GO:0005834; C:heterotrimeric G-protein complex; TAS.
CC GO; GO:0005525; F:GTP binding; TAS.
CC GO; GO:0007189; P:G-protein signaling, adenylate cyclase acti. . . ; TAS.
CC InterPro; IPR001019; P:G-protein signaling, adenylate cyclase acti. . . ; TAS.
CC InterPro; IPR000367; Gprotein_alpha_S.
CC InterPro; IPR011025; GproteinA_insert.
CC Pfam; PF00503; G-alpha; 1.
CC PRINTS; PR00318; GPROTEINA.
CC PRINTS; PR00443; GPROTEINAS.
CC ProDom; PD000281; Gprotein_alpha; 1.
CC ADP-ribosylation; GTP-binding; Lipoprotein; Multigene family;
CC Nucleotide-binding; Palmitate; Transducer.
CC NP_BIND 49 56 GTP (By similarity).
CC NP_BIND 210 214 GTP (By similarity).
CC NP_BIND 279 282 GTP (By similarity).
CC MOD_RES 188 188 ADP-ribosylarginine (by cholera toxin).
CC LIPID 3 3 S-palmitoyl cysteine (By similarity).
CC CONFLICT 70 70 S -> F (in Ref. 1).
CC CONFLICT 90 90 I -> L (in Ref. 1).
CC CONFLICT 94 94 V -> I (in Ref. 1).
CC SEQUENCE 381 AA; 44248 MW; 12063659457994C CRC64;

Query Match 75.5%; Score 1811; DB 1; Length 381;
Best Local Similarity 94.8%; Pred. No. 7.5e-100;
Matches 344; Conservative 9; Mismatches 10; Indels 0; Gaps 0;

QY 96 KEARKVSRGIDRLMDQKRLDQOQTHRLLLGAGESGKSTIVKQMRILHVNPNPEKKQK 155
Db 19 KERREANKKLEKQKQERLAYKATHRLLLGAGESGKSTIVKQMRILHVNPNPEKKQK 78

QY 156 ILDIRKNVKDAIVTVISAMSTIIPPPVPLANPENQFRSDYIKSIAPITDFEYSOEFFDHVK 215
Db 79 ILDIRKNVKDAIVTVISAMSTIIPPPVPLANPENQFRSDYIKSIAPITDFEYSOEFFDHVK 138

QY 216 KLWDEGVKACFERSNEYQLIDCAQYFLERIDSLSVLDVYPTDQDLLRCRVLTSIGIFETR 275
Db 139 KLWDEGVKACFERSNEYQLIDCAQYFLERIDSLSVLDVYPTDQDLLRCRVLTSIGIFETR 198

QY 276 FQVDKYNFHMFDVGGQDERRKWIQCFNDVTAIYVAACSSYNMVIREDNNTNRLRESLD 335
Db 199 FQVDKYNFHMFDVGGQDERRKWIQCFNDVTAIYVAACSSYNMVIREDNNTNRLRESLD 258

QY 336 LFESIWNRLRTISILFLNKQDMLAEKVLACKSKIEDYFFPEYANTVPEDATPDAGED 395
Db 259 LFESIWNRLRTISILFLNKQDMLAEKVLACKSKIEDYFFPEYANTVPEDATPDAGED 318

QY 396 PKVTRAKFFIRDLFLRISTATGDKHYCPHFTCAVDTENIRRVFNDCRDIIQRMHLKQY 455
Db 319 PKVTRAKFFIRDLFLRISTATGDKHYCPHFTCAVDTENIRRVFNDCRDIIQRMHLKQY 378

QY 456 ELL 458
Db 379 ELL 381

RESULT 7
Q6GLL1_XENLA

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ID Q6GLL1 XENLA PRELIMINARY; PRT; 462 AA.
 AC O6GLL1, 2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE LOC43714 protein (fragment).
 GN Name=LOC43714;
 OS Xenopus laevis (African clawed frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae;
 OC Xenopodinae; Xenopus; Xenopus.
 OX NCBI_TaxID=8355;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Brain;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haie H.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldi M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Udén T.B., Tohiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaby S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Vallalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Heiton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalek U., Smailus D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences."
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Brain;
 RX MEDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;
 RA Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
 RA Richardson P.;
 RT "Genetic and genomic tools for Xenopus research: The NIH Xenopus
 RT initiative."
 RL Dev. Dyn. 225:394-391(2002).
 RN [3]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Brain;
 RA Klein S., Gerhard D.S.;
 RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
 DR ENBL; BC074466; AAH74466.1; -, mRNA.
 DR SMR; O6GLL1; 120-459.
 DR GO; GO:000525; F:GTP binding; IEA.
 DR GO; GO:0004871; F:signal transducer activity; IEA.
 DR GO; GO:0007186; P:g-protein coupled receptor protein signalin. . .; IEA.
 DR GO; GO:0007165; P:signal transduction; IEA.
 DR InterPro; IPR011025; GproteinA_insert.
 DR InterPro; IPR001019; Gprotein_alpha.
 DR InterPro; IPR002885; PPR.
 DR Pfam; PF00503; G-alpha; 1.
 DR PRINTS; PR00318; GPROTEINA.
 DR PRODOM; PD000281; Gprotein_alpha; 1.
 DR SMART; SM00275; G_alpha; 1.
 DR TIGRFAMS; TIGR00756; PPR; 1.
 FT NON TER 1
 SQ SEQUENCE 462 AA; 53392 MW; 57EB03C65C17DAF4 CRC64;

Query Match 73.1%; Score 1755; DB 2; Length 462;
 Best Local Similarity 74.5%; Pred. No. 2.1e-96;
 Matches 345; Conservative 32; Mismatches 56; Indels 30; Gaps 4;

QY 15 PGDPCAASEPPEVDAQAPAPALAPVRAA-ARDTARTLLPRGEGSPACARPADK--- 70
 DB 11 PG-----ASQTGDVPCQPRVEQCKPGRGGDADGLVLLQNGGSGESKQHKASKAPH 65
 QY 71 -----PKEKRQRTQELASERAAKEREAVKARKVSRGIDRLMRDQKRD 115
 DB 66 POLQHPHPQHPQHPPLHKGMDKLRLEKEAE-----KEAKVKSKTIDRVLEKQKRE 119
 QY 116 LOOTHRLLLGAGSGKSTIVKQMRILHVGNGPPEKKQKILDIRKNVKDAIVTIVSAMS 175
 DB 120 YKOTHRLLLGAGSGKSTIVKQMRILHVGNGPPEKKQKILDIRKNVKDAIVTIVSAMS 179
 QY 176 TIIPVPLANPENQFRSDYIKSIAPITDPEYSQEFDFHVKKLWDDGKVCACFERSNEYQL 235
 DB 180 TIIPVPLANPENQFRSDYIKSIAPLSDFDYIQEFHQAQKLWDDGKVCACFERSNEYQL 239
 QY 236 IDCAQYFLERIDSVLSVDTPTDQDLLRCRLVTLSGIFETFRQVDKVNFMFVGGQORDER 295
 DB 240 IDCAQYFLERIDSVLSVDTPTDQDLLRCRLVTLSGIFETFRQVDKVNFMFVGGQORDER 299
 QY 296 RKWIOCFNDVTALIVYVACSSYNNMVIREDNNTNRLRESLDLFESINWNLWLTISTILFEL 355
 DB 300 RKWIOCFNDVTALIVYVACSSYNNMVIREDNNTNRLRESLDLFESINWNLWLTISTILFEL 359
 QY 356 NKQDMLAELVLAGSKIEDYFPEYANYTVPEDATPDAGDPKTRAKFFIRDLFLRISTA 415
 DB 360 NKQDMLAELVLAGSKIEDYFPEYANYTVPEDATPDAGDPKTRAKFFIRDLFLRISTA 419
 QY 416 TDGGRHYCPHTCAVDNTENIRRVNDCRDIITQRMHLKQYELL 458
 DB 420 SGRGRHYCPHTCAVDNTENIRRVNDCRDIITQRMHLKQYELL 462
 RESULT 8
 Q90WN6 XENLA PRELIMINARY; PRT; 379 AA.
 ID Q90WN6
 AC Q90WN6;
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE G-protein alpha subunit.
 GN Name=g(alpha)ex2;
 OS Xenopus laevis (African clawed frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae;
 OC Xenopodinae; Xenopus; Xenopus.
 OX NCBI_TaxID=8355;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RX MEDLINE=21479556; PubMed=11596062; DOI=10.1002/cne.1358;
 RA Mezler M., Fleischer J., Conzelmann S., Korch A., Widmayer P.,
 RA Breer H., Boekhoff I.;
 RT "Identification of a nonmammalian G(olf) subtype: Functional role in
 RT olfactory signaling of airborne odors in Xenopus laevis.";
 RL J. Comp. Neurol. 439:400-410(2001).
 DR EMBL; AJ296281; CAC82735.1; -, mRNA.
 DR HSSP; P04896; 1CJU.
 DR SMR; Q90WN6; 37-376.
 DR GO; GO:000525; F:GTP binding; IEA.
 DR GO; GO:0004871; F:signal transducer activity; IEA.
 DR GO; GO:0007186; P:g-protein coupled receptor protein signalin. . .; IEA.
 DR GO; GO:0007165; P:signal transduction; IEA.
 DR InterPro; IPR011025; GproteinA_insert.
 DR InterPro; IPR001019; Gprotein_alpha.
 DR InterPro; IPR002885; PPR.
 DR Pfam; PF00503; G-alpha; 1.
 DR PRINTS; PR00318; GPROTEINA.
 DR PRODOM; PD000281; Gprotein_alpha; 1.
 DR SMART; SM00275; G_alpha; 1.
 DR TIGRFAMS; TIGR00756; PPR; 1.
 SQ SEQUENCE 379 AA; 44366 MW; 06D2D8E1C8918284 CRC64;


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RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Whole;
RA Strausberg R.;
RL Submitted (JUL-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC076540; AAH76540.1; -; mRNA.
DR SMR; Q6DGL5; 35-396.
DR ZFIN; ZDB-GENE-040718-441; zgc:92392.
DR GO; GO:0005525; F:GTP binding; IEA.
DR GO; GO:0004871; P:signal transducer activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; IEA.
DR GO; GO:0007165; P:signal transduction; IEA.
DR InterPro; IPR011025; Gprotein_alpha.
DR InterPro; IPR001019; Gprotein_alpha_insert.
DR InterPro; IPR00367; Gprotein_alpha.
DR InterPro; IPR002885; pPR.
DR Pfam; PF00503; G-alpha; 1.
DR PRINTS; PR00318; GPROTEINAS.
DR ProDom; PD000281; Gprotein_alpha; 1.
DR SMART; SM00275; G_alpha; 1.
DR TIGRFAMs; TIGR00756; pPR; 1.
SQ SEQUENCE 399 AA; 46859 MW; AELAGAB67D6FCAF7 CRC64;

Query Match 67.5%; Score 1620; DB 2; Length 399;
Best Local Similarity 79.1%; Pred. No. 1.9e-88;
Matches 303; Conservative 35; Mismatches 25; Indels 20; Gaps 1;

QY 96 KEARKVSRGIDRLMDQKRDLOQTHRLLLLGAGESGKSTIVKQMRILHVNFGFNAEKKQK 155
DB 17 KAQREANKKIEKQKQERQAYKATHRLLLLGAGESGKSTIVKQMRILHVNFGFNAEKKQK 76

QY 156 ILDIRKNVKDAIVTVSAMSTIIPVPLANPENQFRSDYIKSIAPITDPYISOEFFDHVK 215
DB 77 IQDIRKNVKDAIVTVSAMSTLIPPIPLANPEQOFRIDYIKSIAPISDFYIYQEFFDHAK 136

QY 216 KLWDDGVKACFERSNEYQLIDCAQYFLERIDSVLSVDYTPDQDLLRCRVLTSIGIFETR 275
DB 137 KLWDEGVKACYERSNEYQLIDCAQYFLERIDAVRQSDYTPTDQDLLRCRVLTSIGIFETR 196

QY 276 FOVDKVNFMFDVGGQDERRKWKIQCNDVTAIYVAACSSYNMVRDNNTRLRESLD 335
DB 197 FOVDKVNFMFDVGGQDERRKWKIQCNDVTAIYVAACSSYNMVRDNNTRLRESLD 256

QY 197 FOVDKVNFMFDVGGQDERRKWKIQCNDVTAIYVAACSSYNMVRDNNTRLREALA 256
DB 197 FOVDKVNFMFDVGGQDERRKWKIQCNDVTAIYVAACSSYNMVRDNNTRLREALA 256

QY 336 LFESINNRWLRTISILFLNKQDMLAEKVLAKGSKIEDYFPEYANYTPE----- 386
DB 257 LFRSINNRWLRTISILFLNKQDMLAEKVLAKGSKIEDYFPEYANYTPEKVRKRCVW 316

QY 387 -----DATPDAGEDPKVTRAKFFIRDLFLRISTATGKGKHCYPHFTCAVDTEN 435
DB 317 KRKKRNGEDVSNITPDGDPVTRAKFFIRDFELKISTESGGRHVCYPHFTCAVDTEN 376

QY 436 IRRVFNDCRDIQRMHLKQYELL 458
DB 377 IRRVFNDCRDIQRMHLKQYELL 399

RESULT 11
ID Q5U3H6_BRARE PRELIMINARY; PRT; 379 AA.
AC Q5U3H6;
DT 01-FEB-2005 (TrEMBLrel. 29, Created)
DT 01-FEB-2005 (TrEMBLrel. 29, Last sequence update)
DT 01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
DE zgc:103521.
GN ORFNames=zgc:103521;
OS Brachydanio rerio (zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Ovary;

RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klautner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heich F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Donald M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Whitting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallos D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Ovary;
RA Director MGC Project;
RL Submitted (NOV-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC085540; AAH85540.1; -; mRNA.
DR SMR; Q5U3H6; 35-376.
DR ZFIN; ZDB-GENE-041114-26; zgc:103521.
DR GO; GO:0005525; F:GTP binding; IEA.
DR GO; GO:0004871; P:signal transducer activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; IEA.
DR GO; GO:0007165; P:signal transduction; IEA.
DR InterPro; IPR011025; Gprotein_alpha_insert.
DR InterPro; IPR001019; Gprotein_alpha.
DR InterPro; IPR000367; Gprotein_alpha_S.
DR Pfam; PF00503; G-alpha; 1.
DR PRINTS; PR00318; GPROTEINA.
DR ProDom; PD000281; Gprotein_alpha; 1.
DR SMART; SM00275; G_alpha; 1.
SQ SEQUENCE 379 AA; 44152 MW; BB6E590A0035F07D CRC64;

Query Match 67.0%; Score 1609; DB 2; Length 379;
Best Local Similarity 82.6%; Pred. No. 8e-88;
Matches 300; Conservative 34; Mismatches 29; Indels 0; Gaps 0;

QY 96 KEARKVSRGIDRLMDQKRDLOQTHRLLLLGAGESGKSTIVKQMRILHVNFGFNAEKKQK 155
DB 17 KAQREANKKIEKQKQERQAYKATHRLLLLGAGESGKSTIVKQMRILHVNFGFNAEKKQK 76

QY 156 ILDIRKNVKDAIVTVSAMSTIIPVPLANPENQFRSDYIKSIAPITDPYISOEFFDHVK 215
DB 77 ILDIRKNVKDAIVTVSAMSTLIPPIPLANPEQOFRIDYIKSIAPISDFYIYQEFFDHAK 136

QY 216 KLWDDGVKACFERSNEYQLIDCAQYFLERIDSVLSVDYTPDQDLLRCRVLTSIGIFETR 275
DB 137 HLWDDGVKACFERSNEYQLIDCAQYFLERIESVRQNDYTPDQDLLRCRVLTSIGIFETR 196

QY 276 FOVDKVNFMFDVGGQDERRKWKIQCNDVTAIYVAACSSYNMVRDNNTRLRESLD 335
DB 197 FOVDKVNFMFDVGGQDERRKWKIQCNDVTAIYVAACSSYNMVRDNNTRLRESLD 256

QY 336 LFESINNRWLRTISILFLNKQDMLAEKVLAKGSKIEDYFPEYANYTPEATPDGAG 395
DB 257 LFRSINNRWLRTISILFLNKQDMLAEKVLAKGSKIEDYFPEYANYTPEATPDGAG 316

QY 396 PKVTRAKFFIRDLFLRISTATGKGKHCYPHFTCAVDTENIRRVNDCRDIQRMHLKQY 455
DB 317 PKVTRAKFFIRDFELKISTASGTDKHCYPHFTCAVDTENIRRVNDCRDIQRMHLKQY 376

QY 456 ELL 458
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Db 377 ELL 379

RESULT 12
Q5FWY2_HUMAN
ID Q5FWY2_HUMAN PRELIMINARY; PRT; 485 AA.
AC Q5FWY2
DT 10-MAY-2005 (TrEMBLrel. 30, Created)
DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
DE GNAS protein (Fragment).
GN Name=GNAS;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Breast;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Scapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Uedin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Paney J., Helton E., Kettner M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Kzywinski M.I., Skalska U., Smalusz D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Breast;
RA Director JGC Project;
RL Submitted (JAN-2005) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC089157; AAH89157.1; -; mRNA.
DR GO; GO:0005525; F:GTP binding; IEA.
DR GO; GO:0004871; F:signal transducer activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. .; IEA.
DR GO; GO:0007165; P:signal transduction; IEA.
DR InterPro; IPR011025; Gprotein insert.
DR InterPro; IPR001019; Gprotein_alpha.
DR InterPro; IPR000367; Gprotein_alpha_S.
DR Pfam; PF00503; G-alpha; 1.
DR PRINTS; PR00318; GPROTEIN.
DR PRINTS; PR00443; GPROTEINAS.
DR PDfam; PD000281; Gprotein_alpha; 1.
DR SMART; SM00275; G_alpha; 1.
FT NON_TER
SQ
SEQUENCE 485 AA; 54745 MW; 0CF4E28B9E52A1A5 CRC64;

Query Match
Best Local Similarity 65.3%; Score 1567.5; DB 2; Length 485;
Matches 308; Conservative 48; Mismatches 89; Indels 23; Gaps 5;

QY 8 RPLFGGDDPCAAEPVVEDAQAPALAPVRAAARDTARTLL-----PRG 56
Db 24 RPLRGK-----AARAPRSDRHPPLPARPRAP-RPAARSPRRALLAEEPSRPARPPGA 77
QY 57 GEGSPACARPKADPKPKKORTQLSNAE-----ERAAKEREAVKARKVSGIDRLMRD 111
Db 78 APALPARVPAPAAAAARPPAAAAAAMGCLGNSKTEDQORNEEKAQREANKKIEKLOK 137

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QY 112 QKRDLOOQTHRLLLLGAGSGSKSTIVKQMRILHVNNGNPE-EKKQKILDIRKNVDAIVTI 170
Db 138 DKQYVRATHRLLLLGAGSGSKSTIVKQMRILHVNNGNPESEKATPKVQDIKNLKEAIEI 197
QY 171 VSRMSTIIPVPLANPENQFRSDYIKSIAPITDPEYSQEFFDHVKLWDDGVKACPFERS 230
Db 198 VAMSNLVPPVELANPENQFRVDYILVMVPPDFPFPEYEHAKALWEDEGVACPFERS 257
QY 231 NEYQLIDCAQYFLERIDSVSLVDYPTDQDLRLCRVLTSIGIFETRFOVDKVNHFMDVGG 290
Db 258 NEYQLIDCAQYFLDKIDVIKQADYVPSDQDLRLCRVLTSIGIFETRFOVDKVNHFMDVGG 317
QY 291 ORDERRKWIOCFNDVTAIIIVAACSSYNMVIREDNNTNRLRESLDLPESINNRWLRTIS 350
Db 318 ORDERRKWIOCFNDVTAIIIFVASSSYNMVIREDNQTNRLQALNPFKSIWNRWLRTIS 377
QY 351 IILFLNKKQDLMLAEKVLGKSKIEDYPEPEYANYTVPEDATPDAGEDPKVTRAKYFIRDLFL 410
Db 378 VIILFNKKQDLMLAEKVLGKSKIEDYPEPEYANYTVPEDATPDAGEDPKVTRAKYFIRDLFL 437
QY 411 RISTATGDGKHGYCPHFTCAVDTENIRRVFNDCCRDIIQRMHLKQYELL 458
Db 438 RISTASGDGKHGYCPHFTCAVDTENIRRVFNDCCRDIIQRMHLKQYELL 485

RESULT 13
Q5JWF1_HUMAN
ID Q5JWF1_HUMAN PRELIMINARY; PRT; 722 AA.
AC Q5JWF1
DT 10-MAY-2005 (TrEMBLrel. 30, Created)
DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE GNAS complex locus.
GN Name=GNAS; ORFNames=RP4-543J19.6-009;
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Laird G.;
RL Submitted (MAY-2005) to the EMBL/GenBank/DBJ databases.
RN [2]
RP NUCLEOTIDE SEQUENCE.
RA Lloyd D.;
RL Submitted (MAY-2005) to the EMBL/GenBank/DBJ databases.
RN [3]
RP NUCLEOTIDE SEQUENCE.
RA Moore M.;
RL Submitted (MAY-2005) to the EMBL/GenBank/DBJ databases.
DR EMBL; AL109840; CAI42933.1; -; Genomic DNA.
DR EMBL; AL132655; CAI43074.1; -; Genomic DNA.
DR EMBL; AL121917; CAI42567.1; -; Genomic DNA.
DR EMBL; AL109840; CAI43074.1; JOINED; Genomic DNA.
DR EMBL; AL121917; CAI43074.1; JOINED; Genomic DNA.
DR EMBL; AL121917; CAI42933.1; JOINED; Genomic DNA.
DR EMBL; AL132655; CAI42933.1; JOINED; Genomic DNA.
DR EMBL; AL109840; CAI42567.1; JOINED; Genomic DNA.
DR EMBL; AL132655; CAI42567.1; JOINED; Genomic DNA.
DR SMR; Q5JWF1; 379-719.
DR Ensembl; ENSG0000087460; Homo sapiens.
DR GO; GO:0005525; F:GTP binding; IEA.
DR GO; GO:0004871; F:signal transducer activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. .; IEA.
DR GO; GO:0007165; P:signal transduction; IEA.
DR InterPro; IPR001019; Gprotein_alpha_bd.
DR InterPro; IPR000367; Gprotein_alpha_S.
DR InterPro; IPR011025; Gprotein_alpha_insert.
DR Pfam; PF00503; G-alpha; 1.
DR PRINTS; PR00318; GPROTEINA.

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DR PRINTS; PR000443; GPROTEINAS.
DR ProDom; PD000281; Gprotein_alpha; 1.
DR SMART; SM00275; G_alpha; 1.
DR TIGRFAMs; TIGR00756; PPR; 1.
SQ SEQUENCE 722 AA; 78821 MW; EC72702CCE835A90 CRC64;

Query Match 65.1%; Score 1563; DB 2; Length 722;
Best Local Similarity 70.7%; Pred. No. 9.5e-85;
Matches 299; Conservative 50; Mismatches 68; Indels 6; Gaps 4;

QY 42 RAAARDTARTLLPR---GGEGSPACARPKADKP-KEKRQTEQLSAEEREAAKEREAVKE 97
DB 300 RKQPNLLNLFVQAFGCGFGRSESPQKASRLKVKVPLAEKRRQMRKEALEKRAQKR 359
QY 98 A-RKVSRIIDRLMDQKEDLQOQTHRLLLLGAGSGSKSTIVKQMRILHVGFNPE-EKKQK 155
DB 360 AEKRSKLIDKQLQDEKMGVMCTHRLLLLGAGSGSKSTIVKQMRILHVGFNPGDSEKATK 419
QY 156 ILDIRKNVKDAIVTVSAMSTIIPVPLANPENQFSDYIKSIAPITDPEYSQEFDFHVK 215
DB 420 VQDIKNLKEAETIVAAASNLPVVELANPENQFVDYILSVNVPDFDFPFPEYEHAK 479
QY 216 KLMDDEGVKACFERSNEYQLIDCAQYFLERIDSLSVDYITPTDQDLRCRVLTSGIFETR 275
DB 480 ALMEDEGVACYSERSNEYQLIDCAQYFLDKIDVIKQADYVPSDQDLRCRVLTSGIFETK 539
QY 276 FOVDKVNFMFDVGGQDERRKWIQCFNDVTAIIVVAACSSYNMVRBNDNTNRLRESLD 335
DB 540 FOVDKVNFMFDVGGQDERRKWIQCFNDVTAIIVVAACSSYNMVRBNDNTNRLRESLD 599
QY 336 LFSIWNRRWLRTISILFLNKQDLAEKVLGAGSKIEDYFPEYANVTVPEDATPDAGED 395
DB 600 LFSIWNRRWLRTISILFLNKQDLAEKVLGAGSKIEDYFPEYARVTTPEATPDAGED 659
QY 396 PKVTRAKFFIRDLFLRISTATGDKGHYCYPHFTCAVDTENIRRVNDCRDIIRQMLKQY 455
DB 660 PVTRAKYFIRDFLRISTASGDGRHYCYPHFTCAVDTENIRRVNDCRDIIRQMLRQY 719
QY 456 ELL 458
DB 720 ELL 722

RESULT 14
Q5JWF2_HUMAN PRELIMINARY; PRT; 736 AA.
AC Q5JWF2;
DT 10-MAY-2005 (TrEMBLrel. 30, Created)
DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE GNAS complex locus.
GN Name=Gnas; ORFNames=RP4-543J19.6-001;
OS Homo sapiens (Human)
OC Eukaryota; Metazoa;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominoidea;
OC Homo
OC NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Laird G.;
RL Submitted (MAY-2005) to the EMBL/GenBank/DBJ databases.
RN [2]
RP NUCLEOTIDE SEQUENCE.
RA Lloyd D.;
RL Submitted (MAY-2005) to the EMBL/GenBank/DBJ databases.
RN [3]
RP NUCLEOTIDE SEQUENCE.
RA Moore M.;
RL Submitted (MAY-2005) to the EMBL/GenBank/DBJ databases.
DR EMBL; AL121917; CAI42566.1; -; Genomic DNA.
DR EMBL; AL132655; CAI43073.1; -; Genomic DNA.
DR EMBL; AL109840; CAI42932.1; -; Genomic DNA.
DR EMBL; AL109840; CAI42566.1; JOINED; Genomic DNA.

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DR EMBL; AL132655; CAI42566.1; JOINED; Genomic DNA.
DR EMBL; AL109840; CAI43073.1; JOINED; Genomic DNA.
DR EMBL; AL121917; CAI43073.1; JOINED; Genomic DNA.
DR EMBL; AL132655; CAI42932.1; JOINED; Genomic DNA.
DR EMBL; AL121917; CAI42932.1; JOINED; Genomic DNA.
DR SMR; Q5JWF2; 379-733.
DR GO; GO:0005525; F:GTP binding; IEA.
DR GO; GO:0004871; F:signal transducer activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. .; IEA.
DR GO; GO:0007165; P:signal transduction; IEA.
DR InterPro; IPR011025; GproteinA_insert.
DR InterPro; IPR001019; Gprotein_alpha.
DR InterPro; IPR000367; Gprotein_alpha_s.
DR InterPro; IPR002885; PPR.
DR Pfam; PF00503; G_alpha; 1.
DR PRINTS; PR00318; GPROTEINA.
DR PRINTS; PR00443; GPROTEINAS.
DR ProDom; PD000281; Gprotein_alpha; 1.
DR SMART; SM00275; G_alpha; 1.
DR TIGRFAMs; TIGR00756; PPR; 1.
SQ SEQUENCE 736 AA; 80219 MW; BD2B6D9A8D00859F CRC64;

Query Match 65.0%; Score 1559; DB 2; Length 736;
Best Local Similarity 68.6%; Pred. No. 1.7e-84;
Matches 300; Conservative 49; Mismatches 68; Indels 20; Gaps 4;

QY 42 RAAARDTARTLLPR---GGEGSPACARPKADKP-KEKRQTEQLSAEEREAAKEREAVKE 97
DB 300 RKQPNLLNLFVQAFGCGFGRSESPQKASRLKVKVPLAEKRRQMRKEALEKRAQKR 359
QY 98 A-RKVSRIIDRLMDQKEDLQOQTHRLLLLGAGSGSKSTIVKQMRILHVGFNPE----- 150
DB 360 AEKRSKLIDKQLQDEKMGVMCTHRLLLLGAGSGSKSTIVKQMRILHVGFNPGDSEKATK 419
QY 151 -----EKKQKILDIRNVKDAIVTVSAMSTIIPVPLANPENQFSDYIKSIAP 201
DB 420 QAARSNSDGEKATKVQDIKNLKEAETIVAAASNLPVVELANPENQFVDYILSVN 479
QY 202 TDFEYSQEFDFHVKLWDDEGVKACFERSNEYQLIDCAQYFLERIDSLSVDYITPTDQDL 261
DB 480 PDFDFPFPEYEHAKALMEDEGVACYSERSNEYQLIDCAQYFLDKIDVIKQADYVPSDQDL 539
QY 262 LRCRVLTSGIFETRFQVDKVNFMFDVGGQDERRKWIQCFNDVTAIIVVAACSSYNMVI 321
DB 540 LRCRVLTSGIFETRFQVDKVNFMFDVGGQDERRKWIQCFNDVTAIIVVAACSSYNMVI 599
QY 322 REDNTNRLRESLDLFPESIWNRRWLRTISILFLNKQDLAEKVLGAGSKIEDYFPEYAN 381
DB 600 REDNTNRLQELALNFKSIWNRRWLRTISILFLNKQDLAEKVLGAGSKIEDYFPEYAN 659
QY 382 YTVPEATPDAGEDPKVTRAKFFIRDLFLRISTATGDKGHYCYPHFTCAVDTENIRRVFN 441
DB 660 YTVPEATPDAGEDPKVTRAKFFIRDLFLRISTATGDKGHYCYPHFTCAVDTENIRRVFN 719
QY 442 DCRDIIRQMLKQYELL 458
DB 720 DCRDIIRQMLRQYELL 736

RESULT 15
Q9ZIN8_MOUSE PRELIMINARY; PRT; 756 AA.
ID Q9ZIN8_MOUSE PRELIMINARY;
AC Q9ZIN8;
DT 01-MAY-1999 (TrEMBLrel. 10, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE G-protein Xlalphas.
GN Name=Gnas;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;

```

	[1]	
RN	NUCLEOTIDE SEQUENCE.	
RP	STRAIN=C57BL;	
RC	MEDLINE=20511925; PubMed=10931851; DOI=10.1074/jbc.M006594200;	
RA	Klemke M., Pasolli H.A., Kehlenbach R.H., Offermanns S., Schultz G.,	
RX	Huttner W.B.;	
RA	"Characterization of the extra-large G protein alpha-subunit Xlalphas.	
RT	II. Signal transduction properties.";	
RL	J. Biol. Chem. 275:33633-33640(2000).	
DR	EWBL; AF116268; AAD14686.1; -, mRNA.	
DR	HSSP; P04896; IAZT.	
DR	SNR; Q9ZIN8; 413-753.	
DR	Ensembl; ENSMUSG00000027523; Mus musculus.	
DR	MGI; MGI:95777; Gnas.	
DR	GO; GO:0005834; C:heterotrimeric G-protein complex; TAS.	
DR	GO; GO:0005624; C:membrane fraction; IMP.	
DR	GO; GO:0003924; F:GTPase activity; TAS.	
DR	GO; GO:0006112; P:energy reserve metabolism; IMP.	
DR	GO; GO:0007186; P:G-protein coupled receptor protein signaling. ; TAS.	
DR	GO; GO:0007189; P:G-protein signaling, adenylate cyclase acti. ; IDA.	
DR	GO; GO:0042493; P:response to drug; IMP.	
DR	InterPro; IPRO11025; GproteinA insert.	
DR	InterPro; IPRO01019; Gprotein_alpha.	
DR	InterPro; IPRO00367; Gprotein_alpha_S.	
DR	InterPro; IPRO02885; PPR.	
DR	Pfam; PF00503; G-alpha; 1.	
DR	PRINTS; PR00318; GPROTEINA.	
DR	PRINTS; PR00443; GPROTEINAS.	
DR	ProDom; PD000281; Gprotein_alpha; 1.	
DR	SMART; SM00275; G_alpha; 1.	
DR	TIGRFAMS; TIGR00756; PPR; 1.	
SQ	SEQUENCE 756 AA; 82302 MW; CA23C896C0E0B0CC CRC64;	
	Query Match 65.0%; Score 1559; DB 2; Length 756;	
	Best Local Similarity 72.6%; Pred. No. 1.7e-84;	
	Matches 292; Conservative 48; Mismatches 60; Indels 2; Gaps 2;	
QY	59 GSPACARPKADKP-KKKQRTEQLSAEREAAKEAREAVKSRGIDRMLDOKEDLQ 117	
DB	355 GLSECTRSRLSPGAKDPMEERKKQMKRKAEIEMREQKADKKSKULDKOLEEEKMDYM 414	
QY	118 QTHRLLLLGAGESGSTIVKQMRILHVGNFPE-EKKQKILDIRKNVKDAIVTVSAMST 176	
DB	415 CTHRLLLLGAGESGSTIVKQMRILHVGNGDSEKATKVQDIKNLKEALETIVAAMSN 474	
QY	177 IIPVPVLANPENQPSRYIKSIAPITDFEYSQEPFDHVKKLWDDGVKAFERSNEYOLI 236	
DB	475 LVPPVELANPENQPRVDYILLVMNPVDFPFPEFYEHAKEALWEDEVGRACVERSNAYOLI 534	
QY	237 DCAQYFLERIDSLSLVDTYTTDDQLLCRVLTSGIFETRQVDKVNFMFDMVGQDERR 296	
DB	535 DCAQYFLDKIDVTIQADYVPSDQLLCRVLTSGIFETKFQVDKVNFMFDMVGQDERR 594	
QY	297 KWTQCNDVTAIYYVAACSSVMNVIREDDNTNRLESDDLFPESINNNRWLRITISILPLN 356	
DB	595 KWTQCNDVTALIFVASSVMNVIREDNQTNRLOEALNLFKSIWNWRWLRITSVLPLN 654	
QY	357 KDQMLAEKVLAGSKIEDYPFEYANYTVPEDATPDAGEDPKVTRAKFFIRDLFLRISTAT 416	
DB	655 KDQLLAEKVLAGSKIEDYPEPARYTTPEDATPECPGEDPRVTRAKYFIRDEFIRSTAS 714	
QY	417 GDGHXYCHPHFTCAVDTENIRRVNDCRDIIQMHLAQYELL 458	
DB	715 GDGHXYCHPHFTCAVDTENIRRVNDCRDIIQMHLAQYELL 756	

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GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: March 2, 2006, 19:30:47 ; Search time 35.591 Seconds
(without alignments)
1063.905 Million cell updates/sec

Title: US-10-618-320A-1
Perfect score: 2400
Sequence: 1 MGLCYSLRPLLCGPGDDPC.....VFNDRCRDIQRMHLKQYELL 458

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA.*

- 1: /cgn2_6/ptodata/1/iaa/5_COMB.pep.*
- 2: /cgn2_6/ptodata/1/iaa/6_COMB.pep.*
- 3: /cgn2_6/ptodata/1/iaa/H_COMB.pep.*
- 4: /cgn2_6/ptodata/1/iaa/PTUS_COMB.pep.*
- 5: /cgn2_6/ptodata/1/iaa/RE_COMB.pep.*
- 6: /cgn2_6/ptodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1819	75.8	388	2	US-09-949-016-9025
2	1559	65.0	781	2	US-09-949-016-9170
3	1529.5	63.7	800	2	US-08-307-896-1
4	1526.5	63.6	926	2	US-10-314-048A-104
5	1525.5	63.6	394	4	PCT-US95-11808-1
6	1525.5	63.6	869	2	US-10-314-048A-100
7	1522	63.4	775	2	US-09-513-838-6
8	1520.5	63.4	394	2	US-09-442-349A-106
9	1520.5	63.4	1181	2	US-09-826-509-587
10	1464.5	61.0	380	2	US-09-949-016-9251
11	808.5	33.7	374	2	US-09-442-349A-4
12	805.5	33.6	374	2	US-09-442-349A-64
13	805.5	33.6	374	2	US-09-442-349A-70
14	803.5	33.5	374	2	US-09-442-349A-66
15	803.5	33.5	374	2	US-09-442-349A-68
16	803.5	33.5	374	2	US-09-442-349A-69
17	802.5	33.4	374	2	US-09-442-349A-65
18	802.5	33.4	374	2	US-09-442-349A-67
19	802.5	33.4	374	2	US-09-442-349A-76
20	800.5	33.4	374	2	US-09-442-349A-72
21	800.5	33.4	374	2	US-09-442-349A-74
22	800.5	33.4	374	2	US-09-442-349A-75
23	800.5	33.4	374	2	US-09-442-349A-82
24	799.5	33.3	374	2	US-09-442-349A-71
25	799.5	33.3	374	2	US-09-442-349A-79
26	799.5	33.3	374	2	US-09-442-349A-85
27	798.5	33.3	374	2	US-09-442-349A-80

28	798.5	33.3	374	2	US-09-442-349A-81	Sequence 81, Appl
29	797.5	33.2	374	2	US-09-442-349A-77	Sequence 77, Appl
30	797.5	33.2	374	2	US-09-442-349A-78	Sequence 78, Appl
31	797.5	33.2	374	2	US-09-442-349A-83	Sequence 83, Appl
32	797.5	33.2	374	2	US-09-442-349A-84	Sequence 84, Appl
33	797.5	33.2	374	2	US-09-442-349A-90	Sequence 90, Appl
34	796.5	33.2	374	2	US-09-442-349A-73	Sequence 92, Appl
35	796.5	33.2	374	2	US-09-442-349A-92	Sequence 93, Appl
36	795.5	33.1	374	2	US-09-442-349A-87	Sequence 87, Appl
37	795.5	33.1	374	2	US-09-442-349A-89	Sequence 89, Appl
38	794.5	33.1	374	2	US-09-442-349A-86	Sequence 86, Appl
39	794.5	33.1	374	2	US-09-442-349A-88	Sequence 88, Appl
40	794.5	33.1	374	2	US-09-442-349A-91	Sequence 91, Appl
41	745.5	31.1	374	2	US-09-442-349A-3	Sequence 3, Appl
42	742.5	30.9	374	2	US-09-442-349A-35	Sequence 35, Appl
43	742.5	30.9	374	2	US-09-442-349A-41	Sequence 41, Appl
44	740.5	30.9	374	2	US-09-442-349A-37	Sequence 37, Appl
45	740.5	30.9	374	2	US-09-442-349A-39	Sequence 39, Appl

ALIGNMENTS

RESULT 1

US-09-949-016-9025
; Sequence 9025, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CLO01307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9025
; LENGTH: 388
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-9025

Query Match	75.8%	Score 1819;	DB 2;	Length 388;
Best Local Similarity	95.0%	Pred. No. 3.6e-168;		
Matches	345;	Conservative	9;	Mismatches 0; Indels 0; Gaps 0;
QY	96	KEARKVSRGIDRMRLQKRDLOQTHRLLLGAGESGKSTIVKQMRILHVNQFNPEKKQK	155	
DB	26	KERREANKKIEKOLQERLAYKATHRLLLGAGESGKSTIVKQMRILHVNQFNPEKKQK	85	
QY	156	ILDIRKNVKDAIVTVISAMSTIIPVPLANPENQFRSDYIKSIAPITDPYSEFFPDHVK	215	
DB	86	ILDIRKNVKDAIVTVISAMSTIIPVPLANPENQFRSDYIKSIAPITDPYSEFFPDHVK	145	
QY	216	KLWDDGKACFPERSNEYQLIDCAQYFLERIDSVSLVDVYTPPTDQDLCRCRLVTSIGIFETR	275	
DB	146	KLWDDGKACFPERSNEYQLIDCAQYFLERIDSVSLVDVYTPPTDQDLCRCRLVTSIGIFETR	205	
QY	276	FQVDKYNFMFVGGQDERRKWIQCFNDVTALIIYVAACSSYNNMVIREDNNTLRRESLD	335	
DB	206	FQVDKYNFMFVGGQDERRKWIQCFNDVTALIIYVAACSSYNNMVIREDNNTLRRESLD	265	
QY	336	LFESIWNRLRTISILFLNKQDMLEAKVLAGSKIEDYFFPEYANTVPEDATPDAGED	395	
DB	266	LFESIWNRLRTISILFLNKQDMLEAKVLAGSKIEDYFFPEYANTVPEDATPDAGED	325	
QY	396	PKVTRAKFFIRDLFLRISTATGDKGHYCPHFTCAVDTENIRKRVFNDCRDIIQRMHLKQY	455	

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Db 326 PKVTRAKFFIRDLFLRISTATGDKHCYPHFTCAVDTENIRRVFNCRDIIQRMHLKQY 385
Qy 456 ELL 458
Db 386 ELL 388

RESULT 2
US-09-949-016-9170
; Sequence 9170, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9170
; LENGTH: 781
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-9170

Query Match 65.08; Score 1559; DB 2; Length 781;
Best Local Similarity 65.6%; Pred. No. 2e-142;
Matches 300; Conservative 49; Mismatches 68; Indels 20; Gaps 4;

Qy 42 RAAARDTARTLLPR--GSGSPACARPKADKP-KEKRQTEOLSAEEREAAREAVKE 97
Db 345 RKQPNLLRFLVQAFGCGFRSESPQKASRLKVKVPLAEKRQMRKEALEKRAQKR 404
Qy 98 A-RKVSIGIRMLRDQKRLDQTHRLLLGAGSGKSTIVKQMRILHVGPNPE-----150
Db 405 AEKRSKLIDKQLQDEKQGYMCTHRLLLGAGSGKSTIVKQMRILHVGNGEGEEDP 464
Qy 151 -----EKKQKILDIRKNVKDAIVTIVSAMSTIIPVPLANPENQFRSDYIKSIAP 201
Db 465 QAARNSDGEKATKVQDIKNLKEAETIIVAAMSNLVPVVELANPENQFRVDYILSVNV 524
Qy 202 TDFEYSOEFFDHVKKLWDDGKVCACFERSNEYQLIDCAQYFLERIDSVLSVDYTPDQDL 261
Db 525 PFDPPPEFVEHAKALWDEGVRACYSNEYQLIDCAQYFLDKIDVIKQADTVPSDQDL 584
Qy 262 LRCRLVTSGIFETRFQVDKYNFHMFDVGGQDERRRKKWICFNDVTAIIVAAACSSYNNVI 321
Db 585 LRCRLVTSGIFETRFQVDKYNFHMFDVGGQDERRRKKWICFNDVTAIIVFVASSYNNVI 644
Qy 322 REDNNTNRLRESLDLPESINNNRWLRTISILFLNKQDMLAEKVLGAGSKIEDYFPEYAN 381
Db 645 REDNQTNRLOEALNLFKSIWNNRWLRTISVILFLNKQDMLAEKVLGAGSKIEDYFPEFAR 704
Qy 382 YTVPEPATPDAGSDPKVTRAKFFIRDLFLRISTATGDKHCYPHFTCAVDTENIRRVFN 441
Db 705 YTTPEPATPDGSDPRVTRAKYFIRDFELRISTASGDRHRCYPHFTCAVDTENIRRVFN 764
Qy 442 DCRDIIQRMHLKQYELL 458
Db 765 DCRDIIQRMHLKQYELL 781

RESULT 3
US-08-307-896-1
; Sequence 1, Application US/08307896C
```

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; Patent No. 6034071
; GENERAL INFORMATION:
; APPLICANT: Iyengar, Srinivas Ravi
; TITLE OF INVENTION: MUTANT ACTIVATED GSALPHA AND ADENYLYL
; FILE REFERENCE: 29770
; CURRENT APPLICATION NUMBER: US/08/307,896C
; CURRENT FILING DATE: 1994-09-16
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 380
; TYPE: PRT
; ORGANISM: Homo sapiens
US-08-307-896-1

Query Match 63.7%; Score 1529.5; DB 2; Length 380;
Best Local Similarity 76.2%; Pred. No. 5e-140;
Matches 281; Conservative 45; Mismatches 42; Indels 1; Gaps 1;

Qy 91 EREAVKEARKVSRGIDRMRLDQKRLDQTHRLLLGAGSGKSTIVKQMRILHVGPNPE 150
Db 12 QRNEEKAQREANKIEKQLQDKQVYRATHRLLLGAGSGKSTIVKQMRILHVGNGD 71
Qy 151 -EKKQKILDIRKNVKDAIVTIVSAMSTIIPVPLANPENQFRSDYIKSIAPITDPEYSO 209
Db 72 SEKATKVQDIKNLKEAETIIVAAMSNLVPVVELANPENQFRVDYILSVNVDPDFPPE 131
Qy 210 FFDHVKKLWDDGKVCACFERSNEYQLIDCAQYFLERIDSVLSVDYTPDQDLRCRLVLS 269
Db 132 FYEHAKALWDEGVRACYSNEYQLIDCAQYFLDKIDVIKQADYVPSDQDLRCRLVLS 191
Qy 270 GIFETRFQVDKYNFHMFDVGGQDERRRKKWICFNDVTAIIVAAACSSYNNVIREDNNTNR 329
Db 192 GIFETRFQVDKYNFHMFDVGGQDERRRKKWICFNDVTAIIVFVASSYNNVIREDNQTNR 251
Qy 330 LRESLDLPESINNNRWLRTISILFLNKQDMLAEKVLGAGSKIEDYFPEYANTVTPEDAT 389
Db 252 LOEALNLFKSIWNNRWLRTISVILFLNKQDMLAEKVLGAGSKIEDYFPEFARYTTPEAT 311
Qy 390 PDAGSDPKVTRAKFFIRDLFLRISTATGDKHCYPHFTCAVDTENIRRVFNCRDIIQ 449
Db 312 PEPGSDPRVTRAKYFIRDFELRISTASGDRHRCYPHFTCAVDTENIRRVFNCRDIIQ 371
Qy 450 MHLKQYELL 458
Db 372 MHLKQYELL 380

RESULT 4
US-10-314-048A-104
; Sequence 104, Application US/10314048A
; Patent No. 6902902
; GENERAL INFORMATION:
; APPLICANT: Unett, David J.
; APPLICANT: Chen, Ruoping
; APPLICANT: Richman, Jeremy
; APPLICANT: Connolly, Daniel
; APPLICANT: Dang, Huang T.
; APPLICANT: Choi, Bryan
; APPLICANT: Leonard, James
; APPLICANT: Hakak, Yaron
; APPLICANT: Liaw, Chen
; APPLICANT: Lowitz, Kevin P.
; APPLICANT: Behan, Dominic P.
; APPLICANT: Chalmers, Derek T.
; APPLICANT: Lerner, Michael
; TITLE OF INVENTION: Human G Protein-Coupled Receptors and Modulators Thereof
; FILE REFERENCE: 22.US6.CIP
; CURRENT APPLICATION NUMBER: US/10/314,048A
; CURRENT FILING DATE: 2002-12-06
; PRIOR APPLICATION NUMBER: 10/096,511
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; PRIOR FILING DATE: 2002-03-12
; PRIOR APPLICATION NUMBER: 05/995,543
; PRIOR FILING DATE: 2001-11-27
; PRIOR APPLICATION NUMBER: 60/399,917
; PRIOR FILING DATE: 2002-07-29
; PRIOR APPLICATION NUMBER: 60/404,761
; PRIOR FILING DATE: 2002-08-19
; PRIOR APPLICATION NUMBER: 60/410,747
; PRIOR FILING DATE: 2002-09-13
; NUMBER OF SEQ ID NOS: 161
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 104
; LENGTH: 926
; TYPE: PRT
; ORGANISM: Homo sapiens and Rat
; US-10-314-048A-104

Query Match      63.6%; Score 1526.5; DB 2; Length 926;
Best Local Similarity 63.5%; Pred. No. 3.8e-139;
Matches 298; Conservative 51; Mismatches 67; Indels 53; Gaps 5;

QY 24 EPPVEDAQP-----APAPALAPVRAAARDTARTLL-----PRGGEGSPACA 64
DB 477 KPPKEDSHDLPCTEGTEGKIVPSYDSATFPALSAEFHTGLVDSPSSVSLGCRSNGC- 535
QY 65 RPKADPKKQKQTEQLSABEBAKREAVKRGIDRMLRDKQKDLQOQTHRLLL 124
DB 536 ---LGNKSTEDQRNEE-----KAQREANKKIEKQLQKQKVYRATHRLLL 577

QY 125 LGAGESGKSTIVKQMRILHVGNGNPE-----EKKQKILDIRKNVKDAIVT 169
DB 578 LGAGESGKSTIVKQMRILHVGNGEGEEDPQAARSNSDGEKATKVQDIKNLKEAIE 637

QY 170 IVSAMSTIIPVPLANPENFRSDYIKSIAPITDFEYSQEFFDHHVKLWDEGVKACFER 229
DB 638 IVAMSNLVPVELANPENFRVDYIILSVNVPNDFPPPEFYEHAKALWEDEGVACIER 697

QY 230 SNEYQLIDCAQYFLERIDSVSLVDYPTDQDLRLCRVLTSGIFETRFQVDKVNFMFDVG 289
DB 698 SNEYQLIDCAQYFLERIDSVSLVDYPTDQDLRLCRVLTSGIFETRFQVDKVNFMFDVG 757

QY 290 GQDERERKWTQCNVDVTALIIYVAACSSYNMVIREDNNTNRLRESLDLFIWNNRMLRTI 349
DB 758 GQDERERKWTQCNVDVTALIIYVAACSSYNMVIREDNNTNRLRESLDLFIWNNRMLRTI 817

QY 350 SIILFLNKQDLAEKVLAKGSKIEDYYPEVANYTVPEDATPDAGEDPKVTRAKFFIRDLF 409
DB 818 SVILFLNKQDLAEKVLAKGSKIEDYYPEVANYTVPEDATPDAGEDPKVTRAKFFIRDEF 877

QY 410 LRISTATGDKGHYCYPHFTCAVDTENIRRVFNDCRDIIRQMHKQYELL 458
DB 878 LRISTASGDRGHYCYPHFTCAVDTENIRRVFNDCRDIIRQMHKQYELL 926

RESULT 5
PCT-US95-11808-1
; Sequence 1, Application PC/TUS9511808
; GENERAL INFORMATION:
; APPLICANT: Iyengar, Srinivas Ravi V.
; TITLE OF INVENTION: MUTANT ACTIVATED GsALPHA AND
; TITLE OF INVENTION: ADENYL
; CYCLE OF INVENTION: CYCLASE 2 FOR USE AS THERAPEUTIC AGENTS
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Brumbaugh, Graves, Donohue and
; ADDRESSEE: Raymond
; STREET: 30 Rockefeller Plaza
; CITY: New York
; STATE: New York
; COUNTRY: U.S.
; ZIP: 10112-0228
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk

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; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/11808
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/307,896
; FILING DATE: 16-SEP-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Clark, Richard S.
; REGISTRATION NUMBER: 26,154
; REFERENCE/DOCKET NUMBER: 29970 165/28755
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 765-2519
; TELEFAX: (212) 765-2519
; TELEX: 650 6111063
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 394 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ORIGINAL SOURCE:
; ORGANISM: GsALPHA
; PCT-US95-11808-1

Query Match      63.6%; Score 1525.5; DB 4; Length 394;
Best Local Similarity 73.6%; Pred. No. 1.3e-139;
Matches 282; Conservative 44; Mismatches 42; Indels 15; Gaps 1;

QY 91 EREAVAEARKVSRGIDRMLRDKQKDIQOQTHRLLLLGAGESGKSTIVKQMRILHVGNGNPE 150
DB 12 QRNEEKAQREANKKIEKQKQKVYRATHRLLLLGAGESGKSTIVKQMRILHVGNGE 71

QY 151 -----EKKQKILDIRKNVKDAIVTIVSAMSTIIPVPLANPENQFRSDYI 195
DB 72 GGEEDPQAARSNSDGEKATKVQDIKNLKEAIEIIVAMSNLVPVELANPENQFRVDYI 131

QY 196 KSTAPITDFEYSQEFFDHHVKLWDEGVKACFERSENEYQLIDCAQYFLERIDSVSLVDYT 255
DB 132 LSVNVPNDFPPPEFYEHAKALWEDEGVACIERSENEYQLIDCAQYFLERIDSVSLVDYT 191

QY 256 PTQDQLRLCRVLTSGIFETRFQVDKVNFMEDVGGQDERERKWTQCNVDVTALIIYVAACS 315
DB 192 PSDQDLRLCRVLTSGIFETRFQVDKVNFMEDVGGQDERERKWTQCNVDVTALIIYVAACS 251

QY 316 SYNVMVIREDNNTNRLRESLDLFIWNNRMLRTISILFLNKQDLAEKVLAKGSKIEDY 375
DB 252 SYNVMVIREDNNTNRLRESLDLFIWNNRMLRTISILFLNKQDLAEKVLAKGSKIEDY 311

QY 376 FPEYANYTVPEDATPDAGEDPKVTRAKFFIRDLFIWNNRMLRTISILFLNKQDLAEKVLAKGSKIEDY 435
DB 312 FPEYANYTVPEDATPDAGEDPKVTRAKFFIRDLFIWNNRMLRTISILFLNKQDLAEKVLAKGSKIEDY 371

QY 436 IRRVFNDCRDIIRQMHKQYELL 458
DB 372 IRRVFNDCRDIIRQMHKQYELL 394

RESULT 6
US-10-314-048A-100
; Sequence 100, Application US/10314048A
; Patent No. 6902902
; GENERAL INFORMATION:
; APPLICANT: Unett, David J.
; APPLICANT: Chen, Ruoping
; APPLICANT: Richman, Jeremy
; APPLICANT: Connolly, Daniel
; APPLICANT: Dang, Huong T.
; APPLICANT: Choi, Bryan

```

APPLICANT: Leonard, James
APPLICANT: Hakak, Yaron
APPLICANT: Liaw, Chen
APPLICANT: Lowitz, Kevin P.
APPLICANT: Behan, Dominic P.
APPLICANT: Chalmers, Derek T.
APPLICANT: Lerner, Michael
TITLE OF INVENTION: Human G Protein-Coupled Receptors and Modulators Thereof
TITLE OF INVENTION: for the Treatment of Metabolic-Related Disorders
FILE REFERENCE: 22 US6 CIP
CURRENT APPLICATION NUMBER: US/10/314,048A
CURRENT FILING DATE: 2002-12-06
PRIOR APPLICATION NUMBER: 10/096,511
PRIOR FILING DATE: 2002-03-12
PRIOR APPLICATION NUMBER: 09/995,543
PRIOR FILING DATE: 2001-11-27
PRIOR APPLICATION NUMBER: 60/399,917
PRIOR FILING DATE: 2002-07-29
PRIOR APPLICATION NUMBER: 60/404,761
PRIOR FILING DATE: 2002-08-19
PRIOR APPLICATION NUMBER: 60/410,747
PRIOR FILING DATE: 2002-09-13
NUMBER OF SEQ ID NOS: 161
SOFTWARE: PatentIn version 3.1
SEQ ID NO 100
LENGTH: 869
TYPE: PRT
ORGANISM: Homo sapiens and Rat
US-10-314-048A-100

Query Match 63.6%; Score 1525.5; DB 2; Length 869;
Best Local Similarity 60.5%; Pred. No. 4.4e-139;
Matches 302; Conservative 52; Mismatches 70; Indels 75; Gaps 7;
QY 8 RPLFGGDDPCAAEPPVED-----
DB 398 RPL-----PSPKQPPAVDFRIPQIAETSEFLEQOLTSITMSDSYLRPAASPL 449
QY 39 -APVRAARDTA---RLLPRGEGSPACARPADKPKRKQRTQLSAEERAAKERE 94
DB 450 ESAISAEFFHTGLVDPSSVSLGCRSMGC-----LGNSKTEDQNEE----- 491
QY 95 VKBARKVSRGIDRLMRDQKRDLOQTHRLLLGAGESGKSTIVKQMRILHVGFNPE--- 150
DB 492 -KAQREANKKIEKQKQKQVYRATHRLLLGAGESGKSTIVKQMRILHVGENGSGEE 550
QY 151 -----EKQKILDIRKNVDAIVTIVSAMSTIIPVPLANPENQFRSDYIKSTA 199
DB 551 DPQAARSNDGKATKQDQIKNNLKEAETIVAAMSNLVPVELANPENQFRVDYILSYM 610
QY 200 PITDPEYSQEFFDHVKLWDEGVKACFERSNEYQLIDCAQYFLERIDSVSLVDTPTDQ 259
DB 611 NVPNFDFPPEFYEHAKALWEDEGVKACFERSNEYQLIDCAQYFLERIDSVSLVDTPTDQ 670
QY 260 DLRCRVLTSGIPETRFQVDKVNFMFVGGQDERRRKKWIOCFNDVTAILIYVAACSSYNN 319
DB 671 DLRCRVLTSGIPETRFQVDKVNFMFVGGQDERRRKKWIOCFNDVTAILIYVAACSSYNN 730
QY 320 VIREDNNTNRLRESLDFESINWNRWLTISIILFNKQDMLAEKVLGACKSKIEDYFPEY 379
DB 731 VIREDNNTNRLRESLDFESINWNRWLTISIILFNKQDMLAEKVLGACKSKIEDYFPEY 790
QY 380 ANTVVEDATPDAGEDPKVTRAKFFIRDLFLRISTATGDKHYCPHFCAVDTENIRRV 439
DB 791 ARYTTPEDATPEPEDPRVTRAKFYIRDEFRLISTASGDRHYCPHFCAVDTENIRRV 850
QY 440 FNDCRDIIQRMHLKQYELL 458
DB 851 FNDCRDIIQRMHLKQYELL 869

RESULT 7

US-09-513-838-6

Sequence 6, Application US/09513838
Patent No. 6420563
GENERAL INFORMATION:
APPLICANT: Beeley, Nigel R
APPLICANT: Behan, Dominic P
APPLICANT: Chalmers, Derek T
APPLICANT: Menzaghi, Frederique
APPLICANT: Strah-Pleynt, Sonja
TITLE OF INVENTION: Small Molecule Modulators Of G Protein-Coupled Receptor
TITLE OF INVENTION: Six
FILE REFERENCE: AREN0058
CURRENT APPLICATION NUMBER: US/09/513,838
CURRENT FILING DATE: 2000-02-25
EARLIER APPLICATION NUMBER: 09/364,425
EARLIER FILING DATE: 1999-07-30
EARLIER APPLICATION NUMBER: 60/094,879
EARLIER FILING DATE: 1998-07-31
EARLIER APPLICATION NUMBER: 60/106,300
EARLIER FILING DATE: 1998-10-30
EARLIER APPLICATION NUMBER: 60/110,906
EARLIER FILING DATE: 1998-12-04
EARLIER APPLICATION NUMBER: 60/121,851
EARLIER FILING DATE: 1999-02-26
EARLIER APPLICATION NUMBER: 60/173,850
EARLIER FILING DATE: 1999-12-30
EARLIER APPLICATION NUMBER: 60/174,428
EARLIER FILING DATE: 2000-01-04
EARLIER APPLICATION NUMBER: 09/364,425
EARLIER FILING DATE: 1999-07-30
NUMBER OF SEQ ID NOS: 6
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 6
LENGTH: 775
TYPE: PRT
ORGANISM: Homo sapiens
US-09-513-838-6

Query Match 63.4%; Score 1522; DB 2; Length 775;
Best Local Similarity 67.4%; Pred. No. 8e-139;
Matches 289; Conservative 49; Mismatches 57; Indels 34; Gaps 3;
QY 45 ARDTARTLLPRGEGSPACARPADKPKRKQRTQLSAEERAAKEREAVKEARKVSGS 104
DB 366 SRSPSEVRVPSLGRSMGC-----LGNSKTEDQNEE-----KAQREANKK 406
QY 105 IDRLMRDQKRDLOQTHRLLLGAGESGKSTIVKQMRILHVGFNPE----- 150
DB 407 IEKQLQKQKQVYRATHRLLLGAGESGKSTIVKQMRILHVGENGSGEEDPQAARSND 466
QY 151 -EKQKILDIRKNVDAIVTIVSAMSTIIPVPLANPENQFRSDYIKSTAPITDPEYSOE 209
DB 467 GEKATKQDQIKNNLKEAETIVAAMSNLVPVELANPENQFRVDYILSVNVPNDFPPE 526
QY 210 FPDHYKVLWDDGVKACFERSNEYQLIDCAQYFLERIDSVSLVDTPTDQDLRCRVLT 269
DB 527 FYEHAKALWEDEGVKACFERSNEYQLIDCAQYFLERIDSVSLVDTPTDQDLRCRVLT 586
QY 270 GIFETRFQVDKVNFMFVGGQDERRRKKWIOCFNDVTAILIYVAACSSYNNVIREDNNTNR 329
DB 587 GIFETRFQVDKVNFMFVGGQDERRRKKWIOCFNDVTAILIYVAACSSYNNVIREDNNTNR 646
QY 330 LBESLDLDESINWNRWLTISIILFNKQDMLAEKVLGACKSKIEDYFPEYANYTVPEPAT 389
DB 647 LQELNLFKSIWNRWLTISIILFNKQDMLAEKVLGACKSKIEDYFPEYFARYTTPEDAT 706
QY 390 PDAGDDPKVTRAKFFIRDLFLRISTATGDKHYCPHFCAVDTENIRRVFNDCRDIIQR 449
DB 707 PEPGEDPRVTRAKFYIRDEFRLISTASGDRHYCPHFCAVDTENIRRVFNDCRDIIQR 766
QY 450 MHLKQYELL 458
DB 767 MHLRQYELL 775

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QY 217 LWDEGVKACFERSNEYQLIDCAQYFLERIDSVSLVDYPTDQDLLRCRVLTSIGIPETRF 276
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Db 139 LWDEGVACFERSNEYQLIDCAQYFLDKIDVIKQADYVPSDQDLLRCRVLTSIGIPETRF 198

QY 277 QVDKVNPFMDVGGQDERRKWIQCFNDVTAIIVAAACSSYNMVIREDNNTNRLRESLDL 336
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Db 199 QVDKVNPFMDVGGQDERRKWIQCFNDVTAIIVFVASSYNMVIREDNNTNRLQELN 258

QY 337 FESIMNWRWLTISITILFLNKQDLAEKVLAKGSKIEDYEPYANVTVPEDATPDAGEDP 396
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Db 259 FKSIMNWRWLTISVILFLNKQDLAEKVLAKGSKIEDYEPYFARYTTPEDATPEFGEDP 318

QY 397 KVTTRAKFFIRDLRLISTATGDKGHYCPHFTCAVDTENIRRVFNDRCDDIIQRMHLKQYE 456
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Db 319 RVTRAKYFIRDFLRISTASGDRGHYCPHFTCAVDTENIRRVFNDRCDDIIQRMHLRQYE 378

QY 457 LL 458
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Db 379 LL 380

RESULT 11
US-09-442-349A-4
; Sequence 4, Application US/09442349A
; Patent No. 6462178
; GENERAL INFORMATION:
; APPLICANT: Wong, Yung H
; TITLE OF INVENTION: G Protein
; FILE REFERENCE: M99/0101/US
; CURRENT APPLICATION NUMBER: US/09/442,349A
; CURRENT FILING DATE: 1999-11-17
; NUMBER OF SEQ ID NOS: 116
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 374
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: G protein
; OTHER INFORMATION: Chimera
US-09-442-349A-4

Query Match 33.7%; Score 808.5; DB 2; Length 374;
Best Local Similarity 44.0%; Pred. No. 6.3e-70;
Matches 166; Conservative 71; Mismatches 111; Indels 29; Gaps 6;

QY 93 EAVKEARKVSRGIDRMRLDQKRDLOQTHRLLLLGAGESGKSTIVKQMRIHVNFGNPEEK 152
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Db 16 EDEKAAARVDQEIINRILLEKQKQDRGELKLLLLGPGESGKSTFIKQMRIHAGYSEER 75

QY 153 KQKILDIRKNVKDAIVTIVSAMSTIIPPVPLANPENQFRSDYIKSIAP--ITDFEYSQSF 210
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Db 76 KGFRLPLYQNIIVFSMRAMIEAMERL--QIPFSRPSGKHASLVMSQDPYKVTTFE--KRY 131

QY 211 FDHVKKLWDDEGVKACFERSNEYQLIDCAQYFLERIDSVSLVDYPTDQDLLRCRVLTSG 270
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Db 132 AAAMQWLWDAGIRACYERREFFHLDSAVYVLSHLERITEEGYVPTAQDVLRSRPTTG 191

QY 271 IFETRFQVDKVNPFMDVGGQDERRKWIQCFNDVTAIIVAAACSSYNMVIREDNNTNRL 330
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Db 192 INEYCFSVQKTNLRIVDVGQKSERKKWIHCFENVIALIYLASLSYDQCLEENNOENRM 251

QY 331 RESLDLFEFIMNWRWLTISITILFLNKQDLAEKVLAKGSKIEDYEPYANVTVPEDATP 390
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Db 252 KESLALFGTILFELPWFKSTSVILFLNKTDLLEKI--PTSHLATYPPSF----- 298

QY 391 DAGEDPKVTRAKFFIRDLRLIST-----ATGDKGHYCPHFTCAVDTENIRRVFN 441
||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 299 -QGPKQDAEAAKRFILDMYTRMYTCVDGPEGSASGDRGHYCPHFTCAVDTENIRRVFN 357

QY 442 DCRDIIQRMHLKQYELL 458
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Db 358 DCRDIIQRMHLRQYELL 374

RESULT 13
US-09-442-349A-70
; Sequence 70, Application US/09442349A
; Patent No. 6462178
; GENERAL INFORMATION:
; APPLICANT: Wong, Yung H
; TITLE OF INVENTION: G Protein
; FILE REFERENCE: M99/0101/US
; CURRENT APPLICATION NUMBER: US/09/442,349A
; CURRENT FILING DATE: 1999-11-17
; NUMBER OF SEQ ID NOS: 116
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 70
; LENGTH: 374
; TYPE: PRT
; ORGANISM: Artificial Sequence
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Db 358 DCRDIIQRMHLRQYELL 374

RESULT 12
US-09-442-349A-64
; Sequence 64, Application US/09442349A
; Patent No. 6462178
; GENERAL INFORMATION:
; APPLICANT: Wong, Yung H
; TITLE OF INVENTION: G Protein
; FILE REFERENCE: M99/0101/US
; CURRENT APPLICATION NUMBER: US/09/442,349A
; CURRENT FILING DATE: 1999-11-17
; NUMBER OF SEQ ID NOS: 116
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 64
; LENGTH: 374
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: G protein
; OTHER INFORMATION: Chimera
US-09-442-349A-64

Query Match 33.6%; Score 805.5; DB 2; Length 374;
Best Local Similarity 43.8%; Pred. No. 1.2e-69;
Matches 165; Conservative 72; Mismatches 111; Indels 29; Gaps 6;

QY 93 EAVKEARKVSRGIDRMRLDQKRDLOQTHRLLLLGAGESGKSTIVKQMRIHVNFGNPEEK 152
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Db 16 EDEKAAARVDQEIINRILLEKQKQDRGELKLLLLGPGESGKSTFIKQMRIHAGYSEER 75

QY 153 KQKILDIRKNVKDAIVTIVSAMSTIIPPVPLANPENQFRSDYIKSIAP--ITDFEYSQSF 210
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Db 76 KGFRLPLYQNIIVFSMRAMIEAMERL--QIPFSRPSGKHASLVMSQDPYKVTTFE--KRY 131

QY 211 FDHVKKLWDDEGVKACFERSNEYQLIDCAQYFLERIDSVSLVDYPTDQDLLRCRVLTSG 270
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Db 132 AAAMQWLWDAGIRACYERREFFHLDSAVYVLSHLERITEEGYVPTAQDVLRSRPTTG 191

QY 271 IFETRFQVDKVNPFMDVGGQDERRKWIQCFNDVTAIIVAAACSSYNMVIREDNNTNRL 330
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Db 192 INEYCFSVQKTNLRIVDVGQKSERKKWIHCFENVIALIYLASLSYDQCLEENNOENRM 251

QY 331 RESLDLFEFIMNWRWLTISITILFLNKQDLAEKVLAKGSKIEDYEPYANVTVPEDATP 390
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Db 252 KESLALFGTILFELPWFKSTSVILFLNKTDLLEKI--PTSHLATYPPSF----- 298

QY 391 DAGEDPKVTRAKFFIRDLRLIST-----ATGDKGHYCPHFTCAVDTENIRRVFN 441
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Db 299 -QGPKQDAEAAKRFILDMYTRMYTCVDGPEGSASGDRGHYCPHFTCAVDTENIRRVFN 357

QY 442 DCRDIIQRMHLKQYELL 458
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Db 358 DCRDIIQRMHLRQYELL 374

RESULT 13
US-09-442-349A-70
; Sequence 70, Application US/09442349A
; Patent No. 6462178
; GENERAL INFORMATION:
; APPLICANT: Wong, Yung H
; TITLE OF INVENTION: G Protein
; FILE REFERENCE: M99/0101/US
; CURRENT APPLICATION NUMBER: US/09/442,349A
; CURRENT FILING DATE: 1999-11-17
; NUMBER OF SEQ ID NOS: 116
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 70
; LENGTH: 374
; TYPE: PRT
; ORGANISM: Artificial Sequence
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FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: G protein
; OTHER INFORMATION: Chimera
US-09-442-349A-70

Query Match 33.6%; Score 805.5; DB 2; Length 374;
Best Local Similarity 43.8%; Pred. No. 1.2e-69;
Matches 165; Conservative 72; Mismatches 111; Indels 29; Gaps 6;

QY 93 EAVKEARKVSRGIDRLMDKQKRDLOQTHRLLLGAGESGKSTIVKQMRILHVGNFPEEK 152
DB 16 EDEKAAARVDQENIRLLEKQKQDRGELKLLLLGPGESGKSTFIKQMRIIHGAGYSEER 75

QY 153 KQKILDIRKNVDAIVTIVSAMSTIIPVPLANPENQFRSDYIKSIAP--ITDFEYSQEF 210
DB 76 KGRPLVYQNI FVSMRAMIEMERL--QIPFSPESKHASLVMSQDPYKVTTFE--KRY 131

QY 211 FDHVKKLWDDGKACFERSNEYQLIDCAQFYLERIDSVLSVDYPTDQDLRCRVLTSG 270
DB 132 AAAMQWLWRDAGIRACVERREPHLLDSAVYYLSHLERITEEGVYPTAQDVLRSRMTTG 191

QY 271 IFETRFQVDKVNPFHMFVGGQDRERRKWIQCFNDVTAIYVAAACSSNMVIREDDNNTNRL 330
DB 192 INEVCFSVQKTNLRIVDVGQSKSERKKWIHCFENVIALIYLSLSEYDQCLEENQENRM 251

QY 331 RESLDLFESITWNNRWLRTISIIILFLNKQDMLAEKVLGAKSKIEDYFPEYANYTVPEPATP 390
DB 252 KESLALFGTILELPWFKSTSVILFLNKTDLLEKI--PTSHLATYFPSP----- 298

QY 391 DAGEDPKVTRAKPFIRDLFLRIST-----ATGDKGHYCYPHFTCAVDTENIRRVFN 441
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QY 442 DCRDIIOHMLKQYELL 458
DB 358 DCRDIIOHMLKQYELL 374

RESULT 14

US-09-442-349A-66
; Sequence 66; Application US/09442349A
; Patent No. 6462178
; GENERAL INFORMATION:
; APPLICANT: Wong, Yung H
; TITLE OF INVENTION: G Protein
; FILE REFERENCE: M99/0101/US
; CURRENT APPLICATION NUMBER: US/09/442,349A
; CURRENT FILING DATE: 1999-11-17
; NUMBER OF SEQ ID NOS: 116
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 66
; LENGTH: 374
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: G protein
; OTHER INFORMATION: Chimera
US-09-442-349A-66

Query Match 33.5%; Score 803.5; DB 2; Length 374;
Best Local Similarity 43.8%; Pred. No. 1.9e-69;
Matches 165; Conservative 72; Mismatches 111; Indels 29; Gaps 6;

QY 93 EAVKEARKVSRGIDRLMDKQKRDLOQTHRLLLGAGESGKSTIVKQMRILHVGNFPEEK 152
DB 16 EDEKAAARVDQENIRLLEKQKQDRGELKLLLLGPGESGKSTFIKQMRIIHGAGYSEER 75

QY 153 KQKILDIRKNVDAIVTIVSAMSTIIPVPLANPENQFRSDYIKSIAP--ITDFEYSQEF 210
DB 76 KGRPLVYQNI FVSMRAMIEMERL--QIPFSPESKHASLVMSQDPYKVTTFE--KRY 131

QY 211 FDHVKKLWDDGKACFERSNEYQLIDCAQFYLERIDSVLSVDYPTDQDLRCRVLTSG 270

DB 132 AAAMQWLWRDAGIRACVERREPHLLDSAVYYLSHLERITEEGVYPTAQDVLRSRMTTG 191
QY 271 IFETRFQVDKVNPFHMFVGGQDRERRKWIQCFNDVTAIYVAAACSSNMVIREDDNNTNRL 330
DB 192 INEVCFSVQKTNLRIVDVGQSKSERKKWIHCFENVIALIYLSLSEYDQCLEENQENRM 251

QY 331 RESLDLFESITWNNRWLRTISIIILFLNKQDMLAEKVLGAKSKIEDYFPEYANYTVPEPATP 390
DB 252 KESLALFGTILELPWFKSTSVILFLNKTDLLEKI--PTSHLATYFPSP----- 298

QY 391 DAGEDPKVTRAKPFIRDLFLRIST-----ATGDKGHYCYPHFTCAVDTENIRRVFN 441
DB 299 -QQPKQDAEAAKRFILDMYTRMTGCVDPGEGSASGDRHGYCPHFTCAVDTENIRRVFN 357

QY 442 DCRDIIOHMLKQYELL 458
DB 358 DCRDIIOHMLKQYELL 374

RESULT 15

US-09-442-349A-68
; Sequence 68; Application US/09442349A
; Patent No. 6462178
; GENERAL INFORMATION:
; APPLICANT: Wong, Yung H
; TITLE OF INVENTION: G Protein
; FILE REFERENCE: M99/0101/US
; CURRENT APPLICATION NUMBER: US/09/442,349A
; CURRENT FILING DATE: 1999-11-17
; NUMBER OF SEQ ID NOS: 116
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 68
; LENGTH: 374
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: G protein
; OTHER INFORMATION: Chimera
US-09-442-349A-68

Query Match 33.5%; Score 803.5; DB 2; Length 374;
Best Local Similarity 43.8%; Pred. No. 1.9e-69;
Matches 165; Conservative 71; Mismatches 112; Indels 29; Gaps 6;

QY 93 EAVKEARKVSRGIDRLMDKQKRDLOQTHRLLLGAGESGKSTIVKQMRILHVGNFPEEK 152
DB 16 EDEKAAARVDQENIRLLEKQKQDRGELKLLLLGPGESGKSTFIKQMRIIHGAGYSEER 75

QY 153 KQKILDIRKNVDAIVTIVSAMSTIIPVPLANPENQFRSDYIKSIAP--ITDFEYSQEF 210
DB 76 KGRPLVYQNI FVSMRAMIEMERL--QIPFSPESKHASLVMSQDPYKVTTFE--KRY 131

QY 211 FDHVKKLWDDGKACFERSNEYQLIDCAQFYLERIDSVLSVDYPTDQDLRCRVLTSG 270
DB 132 AAAMQWLWRDAGIRACVERREPHLLDSAVYYLSHLERITEEGVYPTAQDVLRSRMTTG 191

QY 271 IFETRFQVDKVNPFHMFVGGQDRERRKWIQCFNDVTAIYVAAACSSNMVIREDDNNTNRL 330
DB 192 INEVCFSVQKTNLRIVDVGQSKSERKKWIHCFENVIALIYLSLSEYDQCLEENQENRM 251

QY 331 RESLDLFESITWNNRWLRTISIIILFLNKQDMLAEKVLGAKSKIEDYFPEYANYTVPEPATP 390
DB 252 KESLALFGTILELPWFKSTSVILFLNKTDLLEKI--PTSHLATYFPSP----- 298

QY 391 DAGEDPKVTRAKPFIRDLFLRIST-----ATGDKGHYCYPHFTCAVDTENIRRVFN 441
DB 299 -QQPKQDAEAAKRFILDMYTRMTGCVDPGEGSASGDRHGYCPHFTCAVDTENIRRVFN 357

QY 442 DCRDIIOHMLKQYELL 458
DB 358 DCRDIIOHMLKQYELL 374

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Job time : 35.591 secs

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OM protein - protein search, using sw model

Run on: March 2, 2006, 19:32:31 ; Search time 208.863 Seconds
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Title: us-10-618-320a-1
Perfect score: 2400
Sequence: 1 MGLCYSLRPLLLFGPGDDPC.....VFNDCRDIQRMILKQYELL 458

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Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA Main.*
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3: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	1847	77.0	351	5	US-10-732-923-8014
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4	1819	75.8	381	5	US-10-215-982-18
5	1819	75.8	381	5	US-10-732-923-7615
6	1819	75.8	381	5	US-10-732-923-8012
7	1819	75.8	381	5	US-10-736-149-5241
8	1811	75.5	381	5	US-10-732-923-7651
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27	1526.5	63.6	388	5	US-10-732-923-8054

28	1526.5	63.6	926	4	US-10-321-807-104	Sequence 104, App
29	1526.5	63.6	926	4	US-10-321-807-104	Sequence 104, App
30	1526.5	63.6	926	4	US-10-314-048A-104	Sequence 104, App
31	1526.5	63.6	926	5	US-10-897-815-104	Sequence 104, App
32	1526.5	63.6	926	5	US-10-930-662-104	Sequence 104, App
33	1525.5	63.6	394	3	US-09-952-680A-13	Sequence 13, Appl
34	1525.5	63.6	394	3	US-09-963-131-194	Sequence 134, Appl
35	1525.5	63.6	394	4	US-10-116-275-187	Sequence 187, App
36	1525.5	63.6	394	4	US-10-352-843-18	Sequence 18, Appl
37	1525.5	63.6	394	5	US-10-215-982-13	Sequence 13, Appl
38	1525.5	63.6	394	5	US-10-684-422-194	Sequence 194, App
39	1525.5	63.6	394	5	US-10-732-923-8017	Sequence 8017, App
40	1525.5	63.6	394	5	US-10-732-923-8019	Sequence 8019, App
41	1525.5	63.6	869	4	US-10-321-807-100	Sequence 100, App
42	1525.5	63.6	869	4	US-10-321-807-100	Sequence 100, App
43	1525.5	63.6	869	4	US-10-314-048A-100	Sequence 100, App
44	1525.5	63.6	869	5	US-10-897-815-100	Sequence 100, App
45	1525.5	63.6	869	5	US-10-930-662-100	Sequence 100, App

ALIGNMENTS

RESULT 1
US-10-732-923-8011
; Sequence 8011, Application US/10732923
; Publication No. US20050108791A1
; GENERAL INFORMATION:
; APPLICANT: Edgerton, Michael D
; TITLE OF INVENTION: TRANSGENIC PLANTS WITH IMPROVED PHENOTYPES
; FILE REFERENCE: 38-15(52796)C
; CURRENT APPLICATION NUMBER: US/10/732,923
; PRIOR FILING DATE: 2003-12-10
; PRIOR APPLICATION NUMBER: 10/310,154
; PRIOR FILING DATE: 2002-12-04
; NUMBER OF SEQ ID NOS: 24149
; SEQ ID NO 8011
; LENGTH: 458
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-732-923-8011

Query Match 100.0%; Score 2400; DB 5; Length 458;					
Best Local Similarity 100.0%; Pred. No. 1.2e-174;					
Matches 458; Conservative 0; Mismatches 0; Indels 0; Gaps 0;					
Qy	1	MGLCYSLRPLLLFGPGDDPCAA	SEPPVEDAQAPAPALAPVRAA	RDARTATLLPRGEGS	60
Db	1	MGLCYSLRPLLLFGPGDDPCAA	SEPPVEDAQAPAPALAPVRAA	RDARTATLLPRGEGS	60
Qy	61	PACARPKADKPKRKORTEQL	SAEEREAAREAVKEARKVSRG	IDRMLDKRDLQOOTH	120
Db	61	PACARPKADKPKRKORTEQL	SAEEREAAREAVKEARKVSRG	IDRMLDKRDLQOOTH	120
Qy	121	RLLLGAGESGKSTIVKQMRIL	HVNGFNPEKKQKILDIRKNV	KDAIVTVISAMSTIIPP	180
Db	121	RLLLGAGESGKSTIVKQMRIL	HVNGFNPEKKQKILDIRKNV	KDAIVTVISAMSTIIPP	180
Qy	181	VPLANPENQPSYIYKSIAPIT	DFEYSQEPFDHVKKLWDDG	EKVACPFERNELIDCAQ	240
Db	181	VPLANPENQPSYIYKSIAPIT	DFEYSQEPFDHVKKLWDDG	EKVACPFERNELIDCAQ	240
Qy	241	YFLERIDSVSLVDYTPTDQ	LLRCRVLTSGIFETRQVDK	VNFHMFVGGQRRERKWIQ	300
Db	241	YFLERIDSVSLVDYTPTDQ	LLRCRVLTSGIFETRQVDK	VNFHMFVGGQRRERKWIQ	300
Qy	301	CFNDVTAIYVAACSSYNNV	IREDDNTNRLRESLDFES	IWNWRWLTISIILFLNKQDM	360
Db	301	CFNDVTAIYVAACSSYNNV	IREDDNTNRLRESLDFES	IWNWRWLTISIILFLNKQDM	360
Qy	361	LAEKVLAKSKIBDYFPEY	ANYTVTPEDATPDAGED	PKVTRAKFFIRDLFLRISTATGDGK	420
Db	361	LAEKVLAKSKIBDYFPEY	ANYTVTPEDATPDAGED	PKVTRAKFFIRDLFLRISTATGDGK	420

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QY 421 HVCYPHFTCAVDTENIRRVFNDKRDIIQRMHLKQYELL 458
|||||
Db 421 HVCYPHFTCAVDTENIRRVFNDKRDIIQRMHLKQYELL 458
|||||

RESULT 2
US-10-732-923-8014
; Sequence 8014, Application US/10732923
; Publication No. US20050108791A1
; GENERAL INFORMATION:
; APPLICANT: Edgerton, Michael D
; TITLE OF INVENTION: TRANSGENIC PLANTS WITH IMPROVED PHENOTYPES
; FILE REFERENCE: 38-15(52796)C
; CURRENT APPLICATION NUMBER: US/10/732,923
; CURRENT FILING DATE: 2003-12-10
; PRIOR APPLICATION NUMBER: 10/310,154
; PRIOR FILING DATE: 2002-12-04
; NUMBER OF SEQ ID NOS: 24149
; SEQ ID NO 8014
; LENGTH: 351
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-732-923-8014

Query Match 77.0%; Score 1847; DB 5; Length 351;
Best Local Similarity 100.0%; Pred. No. 1.4e-132; Indels 0; Gaps 0;
Matches 351; Conservative 0; Mismatches 0;

QY 108 MLRQKRDLDQOQTHRLLLGAGESGKSTIVQMRLHVNFGNPEKKQKILDIRKNVKDAI 167
|||||
Db 1 MLRQKEDLDQOQTHRLLLGAGESGKSTIVQMRLHVNFGNPEKKQKILDIRKNVKDAI 60
|||||

QY 168 VTVSAMSTIIPVPLANPENQFRSDYIKSIAPITDPEYSQEFDFHVKLWDDGKACF 227
|||||
Db 61 VTVSAMSTIIPVPLANPENQFRSDYIKSIAPITDPEYSQEFDFHVKLWDDGKACF 120
|||||

QY 228 ERSNEYQLIDCAQYFLERIDSVLVDTPTDQDLRLCRVLTSGIFETRFQVDKVNHFMD 287
|||||
Db 121 ERSNEYQLIDCAQYFLERIDSVLVDTPTDQDLRLCRVLTSGIFETRFQVDKVNHFMD 180
|||||

QY 288 VGGORDERRKWIQCFNDVTAIIVAACSSYNMVIREDNNTNRLRESLDLPESIWNNRWLR 347
|||||
Db 181 VGGORDERRKWIQCFNDVTAIIVAACSSYNMVIREDNNTNRLRESLDLPESIWNNRWLR 240
|||||

QY 348 TISILFLNKKQDMLAEKVLGAGKSKIEDYFPEYANYTVPEDATPDAGEDPKVTRAKFFIRD 407
|||||
Db 241 TISILFLNKKQDMLAEKVLGAGKSKIEDYFPEYANYTVPEDATPDAGEDPKVTRAKFFIRD 300
|||||

QY 408 LFURISTATGDKGHYCYHPHFTCAVDTENIRRVFNDKRDIIQRMHLKQYELL 458
|||||
Db 301 LFURISTATGDKGHYCYHPHFTCAVDTENIRRVFNDKRDIIQRMHLKQYELL 351
|||||

RESULT 3
US-09-952-680A-18
; Sequence 18, Application US/09952680A
; Publication No. US20030087239A1
; GENERAL INFORMATION:
; APPLICANT: Stanton, Marty
; APPLICANT: Epstein, David
; APPLICANT: Hamaguchi, No. US20030087239Aluko
; TITLE OF INVENTION: Target Activated Biosensor and Methods of Using Same
; FILE REFERENCE: 23239-501
; CURRENT APPLICATION NUMBER: US/09/952,680A
; CURRENT FILING DATE: 2001-09-13
; PRIOR APPLICATION NUMBER: 60/232,454
; PRIOR FILING DATE: 2000-09-13
; NUMBER OF SEQ ID NOS: 75
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 18
; LENGTH: 381
; TYPE: PRT

; ORGANISM: Homo sapiens
US-09-952-680A-18

Query Match 75.8%; Score 1819; DB 3; Length 381;
Best Local Similarity 95.0%; Pred. No. 2.2e-130; Indels 0; Gaps 0;
Matches 345; Conservative 9; Mismatches 9;

QY 96 KEARKVSRGIDRMRLDKRDLDQOQTHRLLLGAGESGKSTIVQMRLHVNFGNPEKKQK 155
|||||
Db 19 KERREANKKIEKQKQERLAYKATHRLLLGAGESGKSTIVQMRLHVNFGNPEKKQK 78
|||||

QY 156 ILDIRKNVKDAIVTVSAMSTIIPVPLANPENQFRSDYIKSIAPITDPEYSQEFDFHVK 215
|||||
Db 79 ILDIRKNVKDAIVTVSAMSTIIPVPLANPENQFRSDYIKSIAPITDPEYSQEFDFHVK 138
|||||

QY 216 KLWDDGKACFERSNEYQLIDCAQYFLERIDSVLVDTPTDQDLRLCRVLTSGIFETR 275
|||||
Db 139 KLWDDGKACFERSNEYQLIDCAQYFLERIDSVLVDTPTDQDLRLCRVLTSGIFETR 198
|||||

QY 276 FOVDKVNHFMDVGGORDERRKWIQCFNDVTAIIVAACSSYNMVIREDNNTNRLRESLD 335
|||||
Db 199 FOVDKVNHFMDVGGORDERRKWIQCFNDVTAIIVAACSSYNMVIREDNNTNRLRESLD 258
|||||

QY 336 LFESIWNNRWLRITISILFLNKKQDMLAEKVLGAGKSKIEDYFPEYANYTVPEDATPDAGED 395
|||||
Db 259 LFESIWNNRWLRITISILFLNKKQDMLAEKVLGAGKSKIEDYFPEYANYTVPEDATPDAGED 318
|||||

QY 396 PKVTRAKFFIRDLFURISTATGDKGHYCYHPHFTCAVDTENIRRVFNDKRDIIQRMHLKQY 455
|||||
Db 319 PKVTRAKFFIRDLFURISTATGDKGHYCYHPHFTCAVDTENIRRVFNDKRDIIQRMHLKQY 378
|||||

QY 456 ELL 458
|||||
Db 379 ELL 381
|||||

RESULT 4
US-10-215-982-18
; Sequence 18, Application US/10215982
; Publication No. US20040219523A1
; GENERAL INFORMATION:
; APPLICANT: Stanton, Martin
; APPLICANT: Epstein, David
; APPLICANT: Hamaguchi, Nobuko
; APPLICANT: Kurz, Markus
; APPLICANT: Keefe, Tony
; APPLICANT: Wilson, Charles
; APPLICANT: Grate, Dilara
; APPLICANT: Marshall, Kristin
; APPLICANT: McCauley, Thomas
; APPLICANT: Kurz, Jeffrey
; TITLE OF INVENTION: NUCLEIC ACID SENSOR MOLECULES AND METHODS OF USING SAME
; FILE REFERENCE: 23239-501 CIP
; CURRENT APPLICATION NUMBER: US/10/215,982
; CURRENT FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: 60/232,454
; PRIOR FILING DATE: 2000-09-13
; PRIOR APPLICATION NUMBER: 09/952,680
; PRIOR FILING DATE: 2001-09-13
; PRIOR APPLICATION NUMBER: 60/311,378
; PRIOR FILING DATE: 2001-08-09
; PRIOR APPLICATION NUMBER: 60/313,932
; PRIOR FILING DATE: 2001-08-21
; PRIOR APPLICATION NUMBER: 60/338,186
; PRIOR FILING DATE: 2001-11-13
; PRIOR APPLICATION NUMBER: 60/349,959
; PRIOR FILING DATE: 2002-01-18
; PRIOR APPLICATION NUMBER: 60/364,486
; PRIOR FILING DATE: 2002-03-13
; PRIOR APPLICATION NUMBER: 60/376,744
; PRIOR FILING DATE: 2002-05-01
; PRIOR APPLICATION NUMBER: 60/367,991
; PRIOR FILING DATE: 2002-03-25
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; PRIOR APPLICATION NUMBER: 60/369,887
; PRIOR FILING DATE: 2002-04-04
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 372
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 18
; LENGTH: 381
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-215-982-18

Query Match      75.8%; Score 1819; DB 5; Length 381;
Best Local Similarity 95.0%; Pred. No. 2.2e-130;
Matches 345; Conservative 9; Mismatches 9; Indels 0; Gaps 0;

Qy 96 KEARKVSRGIDRMRLDQKRDLOQTHRLLLGAGSGSKSTIVKQMRILHVGNFNPEKKQK 155
Db 19 KERREANKKIEKQKERLAYKATHRLLLGAGSGSKSTIVKQMRILHVGNFNPEKKQK 78
Qy 156 ILDIRKNVKDAIVTIVSAMSTIIPVPLANPENQFRSDYIKSIAPITDFFEYSQBFDDHVK 215
Db 79 ILDIRKNVKDAIVTIVSAMSTIIPVPLANPENQFRSDYIKSIAPITDFFEYSQBFDDHVK 138
Qy 216 KLWDEGVKACFERSNEYQLIDCAQYFLERIDSLSVDYPTDQDLRCRVLTSIGIFETR 275
Db 139 KLWDEGVKACFERSNEYQLIDCAQYFLERIDSLSVDYPTDQDLRCRVLTSIGIFETR 198
Qy 276 FOVDKVNPFMDVGGQDERRKWIQCFNDVTAIYVAACSSYNMVIREDNNTNRLRESLD 335
Db 199 FOVDKVNPFMDVGGQDERRKWIQCFNDVTAIYVAACSSYNMVIREDNNTNRLRESLD 258
Qy 336 LFESIWNRRWLRTISILFLNKQDMLAEKVLGKSKIEDYFPEYANTVVPEDATPDAGED 395
Db 259 LFESIWNRRWLRTISILFLNKQDMLAEKVLGKSKIEDYFPEYANTVVPEDATPDAGED 318
Qy 396 PKVTRAKFFIRDLFLRISTATGDKGHYCYPHFTCAVDTENIRRVFNDNCRDIIQRMHLKQY 455
Db 319 PKVTRAKFFIRDLFLRISTATGDKGHYCYPHFTCAVDTENIRRVFNDNCRDIIQRMHLKQY 378
Qy 456 ELL 458
Db 379 ELL 381

RESULT 6
US-10-732-923-8012
; Sequence 8012, Application US/10732923
; Publication No. US20050108791A1
; GENERAL INFORMATION:
; APPLICANT: Edgerton, Michael D
; TITLE OF INVENTION: TRANSGENIC PLANTS WITH IMPROVED PHENOTYPES
; FILE REFERENCE: 38-15(52796)C
; CURRENT APPLICATION NUMBER: US/10/732,923
; PRIOR FILING DATE: 2003-12-10
; PRIOR APPLICATION NUMBER: 10/310,154
; PRIOR FILING DATE: 2002-12-04
; NUMBER OF SEQ ID NOS: 24149
; SEQ ID NO 8012
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-732-923-8012

Query Match      75.8%; Score 1819; DB 5; Length 381;
Best Local Similarity 95.0%; Pred. No. 2.2e-130;
Matches 345; Conservative 9; Mismatches 9; Indels 0; Gaps 0;

Qy 96 KEARKVSRGIDRMRLDQKRDLOQTHRLLLGAGSGSKSTIVKQMRILHVGNFNPEKKQK 155
Db 19 KERREANKKIEKQKERLAYKATHRLLLGAGSGSKSTIVKQMRILHVGNFNPEKKQK 78
Qy 156 ILDIRKNVKDAIVTIVSAMSTIIPVPLANPENQFRSDYIKSIAPITDFFEYSQBFDDHVK 215
Db 79 ILDIRKNVKDAIVTIVSAMSTIIPVPLANPENQFRSDYIKSIAPITDFFEYSQBFDDHVK 138
Qy 216 KLWDEGVKACFERSNEYQLIDCAQYFLERIDSLSVDYPTDQDLRCRVLTSIGIFETR 275
Db 139 KLWDEGVKACFERSNEYQLIDCAQYFLERIDSLSVDYPTDQDLRCRVLTSIGIFETR 198
Qy 276 FOVDKVNPFMDVGGQDERRKWIQCFNDVTAIYVAACSSYNMVIREDNNTNRLRESLD 335
Db 199 FOVDKVNPFMDVGGQDERRKWIQCFNDVTAIYVAACSSYNMVIREDNNTNRLRESLD 258
Qy 336 LFESIWNRRWLRTISILFLNKQDMLAEKVLGKSKIEDYFPEYANTVVPEDATPDAGED 395
Db 259 LFESIWNRRWLRTISILFLNKQDMLAEKVLGKSKIEDYFPEYANTVVPEDATPDAGED 318
Qy 396 PKVTRAKFFIRDLFLRISTATGDKGHYCYPHFTCAVDTENIRRVFNDNCRDIIQRMHLKQY 455
Db 319 PKVTRAKFFIRDLFLRISTATGDKGHYCYPHFTCAVDTENIRRVFNDNCRDIIQRMHLKQY 378
Qy 456 ELL 458
Db 379 ELL 381

RESULT 5
US-10-732-923-7615
; Sequence 7615, Application US/10732923
; Publication No. US20050108791A1
; GENERAL INFORMATION:
; APPLICANT: Edgerton, Michael D
; TITLE OF INVENTION: TRANSGENIC PLANTS WITH IMPROVED PHENOTYPES
; FILE REFERENCE: 38-15(52796)C
; CURRENT APPLICATION NUMBER: US/10/732,923
; CURRENT FILING DATE: 2003-12-10
; PRIOR APPLICATION NUMBER: 10/310,154
; PRIOR FILING DATE: 2002-12-04
; NUMBER OF SEQ ID NOS: 24149
; SEQ ID NO 7615
; LENGTH: 381
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-732-923-7615

Query Match      75.8%; Score 1819; DB 5; Length 381;
Best Local Similarity 95.0%; Pred. No. 2.2e-130;
Matches 345; Conservative 9; Mismatches 9; Indels 0; Gaps 0;

Qy 96 KEARKVSRGIDRMRLDQKRDLOQTHRLLLGAGSGSKSTIVKQMRILHVGNFNPEKKQK 155
Db 19 KERREANKKIEKQKERLAYKATHRLLLGAGSGSKSTIVKQMRILHVGNFNPEKKQK 78
Qy 156 ILDIRKNVKDAIVTIVSAMSTIIPVPLANPENQFRSDYIKSIAPITDFFEYSQBFDDHVK 215
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RESULT 7
US-10-756-149-5241
; Sequence 5241, Application US/10756149
; Publication No. US20050181375A1
; GENERAL INFORMATION:
; APPLICANT: Aziz, Natasha
; APPLICANT: Zlotnik, Albert
; TITLE OF INVENTION: NOVEL METHODS OF DIAGNOSIS OF METASTATIC CANCER, COMPOSITIONS AND
; FILE OF INVENTION: METHODS OF SCREENING FOR MODULATORS OF METASTATIC CANCER
; FILE REFERENCE: file
; CURRENT APPLICATION NUMBER: US/10/756,149
; CURRENT FILING DATE: 2004-01-12
; NUMBER OF SEQ ID NOS: 5818
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 5241
; LENGTH: 381
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-756-149-5241

Query Match 75.8%; Score 1819; DB 5; Length 381;
Best Local Similarity 95.0%; Pred. No. 2.2e-130;
Matches 345; Conservative 9; Mismatches 9; Indels 0; Gaps 0;

QY	96	KEARKVSRGIDRMRLDQKRDLOQTHRLLLLGAGESGKSTIVKQMRILHVNFGNPEKKQK	155
DB	19	KERREANKKIEKQOKERLAYKATHRLLLLGAGESGKSTIVKQMRILHVNFGNPEKKQK	78
QY	156	ILDIRKNVKDAIVTVISAMSTIIPVPLANPENQFRSDYIKSIAPITDPEYSOEFFDHVK	215
DB	79	ILDIRKNVKDAIVTVISAMSTIIPVPLANPENQFRSDYIKSIAPITDPEYSOEFFDHVK	138
QY	216	KLWDDGVKACFERSNEYQLIDCAQYFLERIDSLSVDYPTDQDLLRCRVLTSIGIFETR	275
DB	139	KLWDDGVKACFERSNEYQLIDCAQYFLERIDSLSVDYPTDQDLLRCRVLTSIGIFETR	198
QY	276	FQVDKVNFMFVGGQDERRKWIQCFNDVTAIYVAACSSYNMVIREDNNTNRLRESLD	335
DB	199	FQVDKVNFMFVGGQDERRKWIQCFNDVTAIYVAACSSYNMVIREDNNTNRLRESLD	258
QY	336	LFESIWNRLRTISILFLNKODMLAEKVLAKGSKIETYFPEYANTVPEDATPDAGED	395
DB	259	LFESIWNRLRTISILFLNKODMLAEKVLAKGSKIETYFPEYANTVPEDATPDAGED	318
QY	396	PKVTRAKFFIRDLFLRISTATGDKGHYCYPHFTCAVDTENIRRVFNDCRDIIQRMHLKQY	455
DB	319	PKVTRAKFFIRDLFLRISTATGDKGHYCYPHFTCAVDTENIRRVFNDCRDIIQRMHLKQY	378
QY	456	ELL 458	
DB	379	ELL 381	

RESULT 8
US-10-732-923-7651
; Sequence 7651, Application US/10732923
; Publication No. US20050108791A1
; GENERAL INFORMATION:
; APPLICANT: Edgerton, Michael D
; TITLE OF INVENTION: TRANSGENIC PLANTS WITH IMPROVED PHENOTYPES
; FILE REFERENCE: 38-15(52796)C
; CURRENT APPLICATION NUMBER: US/10/732,923
; CURRENT FILING DATE: 2003-12-10
; PRIOR APPLICATION NUMBER: 10/310,154
; PRIOR FILING DATE: 2002-12-04
; NUMBER OF SEQ ID NOS: 24149
; SEQ ID NO 7651
; LENGTH: 381
; TYPE: PRT
; ORGANISM: Rattus norvegicus
US-10-732-923-7651

Query Match 75.5%; Score 1811; DB 5; Length 381;
Best Local Similarity 94.8%; Pred. No. 8.9e-130;
Matches 344; Conservative 9; Mismatches 10; Indels 0; Gaps 0;

QY	96	KEARKVSRGIDRMRLDQKRDLOQTHRLLLLGAGESGKSTIVKQMRILHVNFGNPEKKQK	155
DB	19	KERREANKKIEKQOKERLAYKATHRLLLLGAGESGKSTIVKQMRILHVNFGNPEKKQK	78
QY	156	ILDIRKNVKDAIVTVISAMSTIIPVPLANPENQFRSDYIKSIAPITDPEYSOEFFDHVK	215
DB	79	ILDIRKNVKDAIVTVISAMSTIIPVPLANPENQFRSDYIKSIAPITDPEYSOEFFDHVK	138
QY	216	KLWDDGVKACFERSNEYQLIDCAQYFLERIDSLSVDYPTDQDLLRCRVLTSIGIFETR	275
DB	139	KLWDDGVKACFERSNEYQLIDCAQYFLERIDSLSVDYPTDQDLLRCRVLTSIGIFETR	198
QY	276	FQVDKVNFMFVGGQDERRKWIQCFNDVTAIYVAACSSYNMVIREDNNTNRLRESLD	335
DB	199	FQVDKVNFMFVGGQDERRKWIQCFNDVTAIYVAACSSYNMVIREDNNTNRLRESLD	258
QY	336	LFESIWNRLRTISILFLNKODMLAEKVLAKGSKIETYFPEYANTVPEDATPDAGED	395
DB	259	LFESIWNRLRTISILFLNKODMLAEKVLAKGSKIETYFPEYANTVPEDATPDAGED	318
QY	396	PKVTRAKFFIRDLFLRISTATGDKGHYCYPHFTCAVDTENIRRVFNDCRDIIQRMHLKQY	455
DB	319	PKVTRAKFFIRDLFLRISTATGDKGHYCYPHFTCAVDTENIRRVFNDCRDIIQRMHLKQY	378
QY	456	ELL 458	
DB	379	ELL 381	

RESULT 9

US-10-732-923-7963
; Sequence 7963, Application US/10732923
; Publication No. US20050108791A1
; GENERAL INFORMATION:
; APPLICANT: Edgerton, Michael D
; TITLE OF INVENTION: TRANSGENIC PLANTS WITH IMPROVED PHENOTYPES
; FILE REFERENCE: 38-15(52796)C
; CURRENT APPLICATION NUMBER: US/10/732,923
; CURRENT FILING DATE: 2003-12-10
; PRIOR APPLICATION NUMBER: 10/310,154
; PRIOR FILING DATE: 2002-12-04
; NUMBER OF SEQ ID NOS: 24149
; SEQ ID NO 7963
; LENGTH: 379
; TYPE: PRT
; ORGANISM: Xenopus laevis
US-10-732-923-7963

Query Match 69.9%; Score 1677; DB 5; Length 379;
Best Local Similarity 86.2%; Pred. No. 1.5e-119;
Matches 313; Conservative 25; Mismatches 25; Indels 0; Gaps 0;

QY	96	KEARKVSRGIDRMRLDQKRDLOQTHRLLLLGAGESGKSTIVKQMRILHVNFGNPEKKQK	155
DB	17	KAQREANKKIEKQOKERLAYKATHRLLLLGAGESGKSTIVKQMRILHVNFGNPEKKQK	76
QY	156	ILDIRKNVKDAIVTVISAMSTIIPVPLANPENQFRSDYIKSIAPITDPEYSOEFFDHVK	215
DB	77	SQDIRKNVKDAIVTVISAMSTIIPVPLANPENQFRSDYIKSIAPITDPEYSOEFFDHVK	136
QY	216	KLWDDGVKACFERSNEYQLIDCAQYFLERIDSLSVDYPTDQDLLRCRVLTSIGIFETR	275
DB	137	KLWDDGVKACFERSNEYQLIDCAQYFLERIDSLSVDYPTDQDLLRCRVLTSIGIFETR	196
QY	276	FQVDKVNFMFVGGQDERRKWIQCFNDVTAIYVAACSSYNMVIREDNNTNRLRESLD	335
DB	197	FQVDKVNFMFVGGQDERRKWIQCFNDVTAIYVAACSSYNMVIREDNNTNRLRESLD	256

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QY 336 LFSIMNNRMLRTISIIILFNKQDMLAEKVLGKSKIEDYFPEYANTVPEDATPDAGED 395
Db 257 LFSIMNNRMLRTISIIILFNKQDMLAEKVLGKSKIEDYFPEYANTVPEDATPDAGED 316
QY 396 PKVTRAKFFIRDLFLRISTATGDKGHYCYPHFTCAVDTENIRRVFNCDCRDIIOHMLKQY 455
Db 317 PKVTRAKFFIRDLFLRISTATGDKGHYCYPHFTCAVDTENIRRVFNCDCRDIIOHMLKQY 376
QY 456 ELL 458
Db 377 ELL 379

RESULT 10
US-09-963-131-184
; Sequence 184, Application US/09963131
; Publication No. US20030224460A1
; GENERAL INFORMATION:
; APPLICANT: Pedersen, Finn Skou
; APPLICANT: Sorensen, Annette Balle
; APPLICANT: Hernandez, Javier Martin
; APPLICANT: Nielsen, Anne Ahlmann
; APPLICANT: Moving, Helle
; TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR LYMPHOMA AND LEUKEMIA
; FILE REFERENCE: 52945200323
; CURRENT APPLICATION NUMBER: US/09/963,131
; CURRENT FILING DATE: 2001-09-24
; PRIOR APPLICATION NUMBER: US 09/668,644
; PRIOR FILING DATE: 2000-09-22
; PRIOR APPLICATION NUMBER: US 09/905,390
; PRIOR FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: US 09/905,491
; PRIOR FILING DATE: 2001-07-13
; NUMBER OF SEQ ID NOS: 215
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 184
; LENGTH: 756
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-963-131-184

Query Match 65.0%; Score 1559; DB 3; Length 756;
Best Local Similarity 72.6%; Pred. No. 4e-110;
Matches 292; Conservative 48; Mismatches 60; Indels 2; Gaps 2;

QY 59 GSPACARPKADKP-KEKQRORTEOLSAEEREAAREAVKRVSGIDRMLDKQKDLQ 117
Db 355 GLSECTRSRLSPGAKDPMEERRKQMKAEIEMREKQKADKRSKLIDKQLEEKMDYM 414
QY 118 QTHRLLLGAGESGKSTIVKQMRILHVGNGFNP-EKKQKILDIRKNVKDAIVTIVSAMST 176
Db 415 CTHRLLLGAGESGKSTIVKQMRILHVGNGFNGDSEKATKQDINKNLKEAIEIIVAAMSN 474
QY 177 IIPVPLANPENQFRSDYIKSIAPITDFEYSQBFHVKLWDDGKACFERSNEYQLI 236
Db 475 LVPPVELANPENQFRVDYILSVNVPNFPDFPEFYEHAHALWEDEGVACRYERSNEYQLI 534
QY 237 DCAQYFLERIDSVLDYPTDODLLRCVLTSGIFETRFQVDKVFHMFDMVGGQDERR 296
Db 535 DCAQYFLDKIDVIKQADYVPSQDQLLRCVLTSGIFETRFQVDKVFHMFDMVGGQDERR 594
QY 297 KWIQCNDVTAIIVVACSSYNMVIREDNNTNRLRESLDFESIMNNRMLRTISIIILFN 356
Db 595 KWIQCNDVTAIIVVASSYNMVIREDNNTNRLQELALNLFKSIWNNRMLRTISIIILFN 654
QY 357 KQDLAEKVLGKSKIEDYFPEYANTVPEDATPDAGEDPKVTRAKFFIRDLFLRISTAT 416
Db 655 KQDLAEKVLGKSKIEDYFPEYANTVPEDATPDAGEDPRVTRAKYFIRDFELRISTAS 714
QY 417 GDGKHVCYPHFTCAVDTENIRRVFNCDCRDIIOHMLKQYELL 458
Db 715 GDGRHYCYPHFTCAVDTENIRRVFNCDCRDIIOHMLKQYELL 756

RESULT 11
US-10-732-923-7617
; Sequence 7617, Application US/10732923
; Publication No. US20050108791A1
; GENERAL INFORMATION:
; APPLICANT: Edgerton, Michael D
; TITLE OF INVENTION: TRANSGENIC PLANTS WITH IMPROVED PHENOTYPES
; FILE REFERENCE: 38-15(52796)C
; CURRENT APPLICATION NUMBER: US/10/732,923
; CURRENT FILING DATE: 2003-12-10
; PRIOR APPLICATION NUMBER: 10/310,154
; PRIOR FILING DATE: 2002-12-04
; NUMBER OF SEQ ID NOS: 24149
; SEQ ID NO 7617
; LENGTH: 756
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-732-923-7617

Query Match 65.0%; Score 1559; DB 5; Length 756;
Best Local Similarity 72.6%; Pred. No. 4e-110;
Matches 292; Conservative 48; Mismatches 60; Indels 2; Gaps 2;

QY 59 GSPACARPKADKP-KEKQRORTEOLSAEEREAAREAVKRVSGIDRMLDKQKDLQ 117
Db 355 GLSECTRSRLSPGAKDPMEERRKQMKAEIEMREKQKADKRSKLIDKQLEEKMDYM 414
QY 118 QTHRLLLGAGESGKSTIVKQMRILHVGNGFNP-EKKQKILDIRKNVKDAIVTIVSAMST 176
Db 415 CTHRLLLGAGESGKSTIVKQMRILHVGNGFNGDSEKATKQDINKNLKEAIEIIVAAMSN 474
QY 177 IIPVPLANPENQFRSDYIKSIAPITDFEYSQBFHVKLWDDGKACFERSNEYQLI 236
Db 475 LVPPVELANPENQFRVDYILSVNVPNFPDFPEFYEHAHALWEDEGVACRYERSNEYQLI 534
QY 237 DCAQYFLERIDSVLDYPTDODLLRCVLTSGIFETRFQVDKVFHMFDMVGGQDERR 296
Db 535 DCAQYFLDKIDVIKQADYVPSQDQLLRCVLTSGIFETRFQVDKVFHMFDMVGGQDERR 594
QY 297 KWIQCNDVTAIIVVACSSYNMVIREDNNTNRLRESLDFESIMNNRMLRTISIIILFN 356
Db 595 KWIQCNDVTAIIVVASSYNMVIREDNNTNRLQELALNLFKSIWNNRMLRTISIIILFN 654
QY 357 KQDLAEKVLGKSKIEDYFPEYANTVPEDATPDAGEDPKVTRAKFFIRDLFLRISTAT 416
Db 655 KQDLAEKVLGKSKIEDYFPEYANTVPEDATPDAGEDPRVTRAKYFIRDFELRISTAS 714
QY 417 GDGKHVCYPHFTCAVDTENIRRVFNCDCRDIIOHMLKQYELL 458
Db 715 GDGRHYCYPHFTCAVDTENIRRVFNCDCRDIIOHMLKQYELL 756

RESULT 12
US-10-732-923-8020
; Sequence 8020, Application US/10732923
; Publication No. US20050108791A1
; GENERAL INFORMATION:
; APPLICANT: Edgerton, Michael D
; TITLE OF INVENTION: TRANSGENIC PLANTS WITH IMPROVED PHENOTYPES
; FILE REFERENCE: 38-15(52796)C
; CURRENT APPLICATION NUMBER: US/10/732,923
; CURRENT FILING DATE: 2003-12-10
; PRIOR APPLICATION NUMBER: 10/310,154
; PRIOR FILING DATE: 2002-12-04
; NUMBER OF SEQ ID NOS: 24149
; SEQ ID NO 8020
; LENGTH: 909
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-732-923-8020

Query Match 65.0%; Score 1559; DB 5; Length 909;
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Best Local Similarity 68.6%; Pred. No. 5.1e-110;		Matches 300; Conservative 49; Mismatches 68; Indels 20; Gaps 4;	
QY	42	RAAARDARTLLPR---GGSGSPACARPKADKP-KEKQRTQEQLSAEEREAAKEREAVKE	97
Db	473	RKQPNLLNLFVQAFCGCGFRSESPQPKASRLKVKVPLAEKRRQMRKEALEKRAQKR	532
QY	98	A-RKVSRGIDRLMDQKRDILQOQTHRLLLLAGESGSKSTIVKQMRILHVNFGFNP	150
Db	533	AEKRSKLIDKQLODEKQKGYMCTHRLLLLAGESGSKSTIVKQMRILHVNFGGEGEEDP	592
QY	151	-----EKKQKILDIRKNVDAIVTIVSAMSTIIPVPPLANPENQFRSDYIKSIAP	201
Db	593	QAARSNSDGEKATKVQDIIKNNLKEALETIVAAASNLVPPVELANPENQFRVDYILSMNV	652
QY	202	TDPEYGOEPDHPVKUWDDSGVACAFERSNEYQLIDCAQYFLERIDSVLVDYTPDQDL	261
Db	653	PDFDFPPEFYEHAHALWEDEBGRVACYSNEYQLIDCAQYFLDKIDVIKQADYVPSDQDL	712
QY	262	LRCRVLTSGIFETRFQVDKYNHEMFDVGGORDERRRKWIQCFNDVTALIIYVAACSSYNMVI	321
Db	713	LRCRVLTSGIFETRFQVDKYNHEMFDVGGORDERRRKWIQCFNDVTALIIYVAACSSYNMVI	772
QY	322	REDNNTNRLRESLDLRESIWNRLRTISILFLNKQDMLAEKVLAKGSKIEDYFPEYAN	381
Db	773	REDNNTNRLQALNLFKSIWNNRLRTISILFLNKQDMLAEKVLAKGSKIEDYFPEFAR	832
QY	382	YTPEDATPDAGEDPKVTRAKFIRDLFLRISTATGDKHYCYPHFTCAVDTENIRRVFN	441
Db	833	YTPEDATPDGDPVTRAKYFIRDFLRISTASGDGRHYCYPHFTCAVDTENIRRVFN	892
QY	442	DCRDIIQRMHLQYELL 458	
Db	893	DCRDIIQRMHLQYELL 909	
RESULT 13			
US-10-732-923-7654			
; Sequence 7654, Application US/10732923			
; Publication No. US20050108791A1			
; GENERAL INFORMATION:			
; APPLICANT: Edgerton, Michael D			
; TITLE OF INVENTION: TRANSGENIC PLANTS WITH IMPROVED PHENOTYPES			
; FILE REFERENCE: 38-15(52796)C			
; CURRENT APPLICATION NUMBER: US/10732,923			
; CURRENT FILING DATE: 2003-12-10			
; PRIOR APPLICATION NUMBER: 10/310,154			
; NUMBER OF SEQ ID NOS: 24149			
; SEQ ID NO 7654			
; LENGTH: 715			
; TYPE: PRT			
; ORGANISM: Rattus norvegicus			
US-10-732-923-7654			
Query Match		64.5%; Score 1548; DB 5; Length 715;	
Best Local Similarity		70.2%; Pred. No. 2.5e-109;	
Matches		292; Conservative 47; Mismatches 61; Indels 16; Gaps 2;	
QY	59	GSPACARPKADKP-KEKQRTQEQLSAEEREAAKEREAVKEARVSRGIDRLMDQKRDQ	117
Db	431	GLSECTRSLSFGKAKDPMEERRKQMRKEAMREKQKADKRSKLIDKQLEEEKWDYM	490
QY	118	QTHRLLLLAGESGSKSTIVKQMRILHVNFGFNP	162
Db	491	CTHRLLLLAGESGSKSTIVKQMRILHVNFGGEGEEDPQAARSNSDGEKATKVQDIKNN	550
QY	163	VKDAIVTIVSAMSTIIPVPPLANPENQFRSDYIKSIAPITDPEYGOEPDHPVKUWDD	222
Db	551	LKEAETIVAAASNLVPPVELANPENQFRVDYILSMNVNPNFDPPEFYEHAHALWEDE	610
QY	223	VKACERSNEYQLIDCAQYFLERIDSVLVDYTPDQDLRLCRVLTSGIFETRFQVDKVN	282
Db	611	VRACERSNEYQLIDCAQYFLDKIDVIKQADYVPSDQDLPRCKRVLTSGIFETRFQVDKVN	670
QY	283	FHMFVGGORDERRRKWIQCFNDVTALIIYVAACSSYNMVIREDNNTNRLRESLDLRESIWN	342
Db	671	FHMFVGGORDERRRKWIQCFNDVTALIIYVAACSSYNMVIREDNNTNRLQALNLFKSIWN	730
QY	343	NRLRTISILFLNKQDMLAEKVLAKGSKIEDYFPEYANVTPEDATPDAGEDPKVTRAK	402
Db	731	NRLRTISILFLNKQDMLAEKVLAKGSKIEDYFPEFARYTTPEDATPDGDPVTRAK	790
QY	403	FTRDLFLRISTATGDKHYCYPHFTCAVDTENIRRVFNDCRDIIQRMHLQYELL 458	
Db	791	YFIRDFLRISTASGDGRHYCYPHFTCAVDTENIRRVFNDCRDIIQRMHLQYELL 846	
RESULT 15			
US-10-732-923-7656			
; Sequence 7656, Application US/10732923			
; Publication No. US20050108791A1			
; GENERAL INFORMATION:			
; APPLICANT: Edgerton, Michael D			

; TITLE OF INVENTION: TRANSGENIC PLANTS WITH IMPROVED PHENOTYPES

; FILE REFERENCE: 38-15(52796)C

; CURRENT APPLICATION NUMBER: US/10/732,923

; CURRENT FILING DATE: 2003-12-10

; PRIOR APPLICATION NUMBER: 10/310,154

; PRIOR FILING DATE: 2002-12-04

; NUMBER OF SEQ ID NOS: 24149

; SEQ ID NO 7656

; LENGTH: 846

; TYPE: PRT

; ORGANISM: Rattus norvegicus

US-10-732-923-7656

Query Match 64.2%; Score 1541; DB 5; Length 846;

Best Local Similarity 70.0%; Pred. No. 1.1e-108;

Matches 291; Conservative 47; Mismatches 62; Indels 16; Gaps 2;

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Qy 59 GSPACARPKADKP-KEKQRTEQLSAEREAREAKREAVKEARKVSRGIDRMRLRQKQDLQ 117
Db 431 GLSECTRSRSLSPGAKDPMERKKQMRKEAWEMREKQKADKRSKLIDKOLEEEKMDYM 490
Qy 118 QTHRLLLIGAGESGSTIVKQMRILHVNGFNPE-----EKKQKILDIRKN 162
Db 491 CTHRLLLIGAGESGSTIVKQMRILHVNGFNGEGEEDPQAARSNSDGEKATKVQDIKN 550
Qy 163 VKDAIVTVSAMSTIIPVPLANPENQFRSDYIKSIAPITDFEYSQEFFDHVKKLWDEG 222
Db 551 LKEAETIVAAMSNLPPVELANPENQFRVDYILSVNVPNFPFPPEFYEHAHALWEDEG 610
Qy 223 VKACFERSNEYQLIDCAQYFLERIDSVSLVDYTTDODLLRCRVLTSGIPETRFQVDKN 282
Db 611 VRACYERSNEYQLIDCAWYFLDKIDIVKQADYVPSDQDLPCRVLTSIGIPETKFQVDKN 670
Qy 283 FHMFVGGQDERRKWKIQCNDVTAIIVAAACSSYNMVIREDNNTNRLRESLDLFSIWN 342
Db 671 FHMFVGGQDERRKWKIQCNDVTAIIFVVAASSYNMVIREDNQTNRLOEALNLFKSIWN 730
Qy 343 NRWLRTISILFLNKQDMLAEKVLGKSKIEDYFPEYANYTVPEDATPDAGEDPKVTRAK 402
Db 731 NRWLRTISVILFLNKQDLAEKVLGKSKIEDYFPEFARYTTPEDATPEGEDPRVTRAK 790
Qy 403 FFIRDLFLRISTATGDKGHYCYPHFTCAVDTENIRRVFNDCRDIIOHMLKQYELL 458
Db 791 YFIRDFLRISTASGDGRHYCYPHFTCAVDTENIRRVFNDCRDIIOHMLRQYELL 846
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Search completed: March 2, 2006, 19:41:16

Job time : 210.863 secs

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OM protein --protein search, using sw model

Run on: March 2, 2006, 19:37:27 ; Search time 15.9223 Seconds
(without alignments)
575.298 Million cell updates/sec

Title: US-10-618-320A-1
Perfect score: 2400
Sequence: 1 MGLCYSLRLLFGCGDDPC.....VFNDRCRIQRMHMKOYELL 458

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 135339 seqs, 20000136 residues

Total number of hits satisfying chosen parameters: 135339

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

D. Database : Published Applications AA_New.*
1: /cgn2_6/ptodata/2/pubppa/US08_NEW_PUB.pap.*
2: /cgn2_6/ptodata/2/pubppa/US06_NEW_PUB.pap.*
3: /cgn2_6/ptodata/2/pubppa/US07_NEW_PUB.pap.*
4: /cgn2_6/ptodata/2/pubppa/PCT_NEW_PUB.pap.*
5: /cgn2_6/ptodata/2/pubppa/US09_NEW_PUB.pap.*
6: /cgn2_6/ptodata/2/pubppa/US10_NEW_PUB.pap.*
7: /cgn2_6/ptodata/2/pubppa/US11_NEW_PUB.pap.*
8: /cgn2_6/ptodata/2/pubppa/US60_NEW_PUB.pap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2400	100.0	458	6	US-10-618-320A-1
2	2124	88.5	448	6	US-10-618-320A-25
3	2113	88.0	450	6	US-10-618-320A-26
4	1538	64.1	864	7	US-11-053-100-58
5	1525.5	63.6	394	6	US-10-821-234-1626
6	728.5	30.4	353	7	US-11-060-023-4
7	728.5	30.4	353	7	US-11-060-023-8
8	723.5	30.1	859	7	US-11-053-100-52
9	723.5	30.1	1309	7	US-11-053-100-53
10	720.5	30.0	353	7	US-11-060-023-15
11	719.5	30.0	359	7	US-11-060-023-13
12	717.5	29.9	353	7	US-11-060-023-12
13	717.5	29.9	353	7	US-11-060-023-14
14	717.5	29.9	359	7	US-11-060-023-11
15	717.5	29.9	360	7	US-11-060-023-17
16	716.5	29.9	353	7	US-11-060-023-16
17	705.5	29.4	353	7	US-11-060-023-2
18	705.5	29.4	353	7	US-11-060-023-6
19	691.5	28.8	408	6	US-10-821-234-1100
20	672.5	28.0	374	7	US-11-060-023-10
21	672.5	28.0	374	7	US-11-228-364-2
22	672.5	28.0	374	7	US-11-159-041-188
23	647.5	27.0	374	7	US-11-228-364-4
24	125.5	5.2	627	7	US-11-150-845-47
25	122	5.1	179	7	US-11-093-746A-25

ALIGNMENTS

RESULT 1
US-10-618-320A-1
; Sequence 1, Application US/10618320A
; Publication No. US20050260595A1
; GENERAL INFORMATION:
; APPLICANT: Sumitomo Chemical Company Limited
; TITLE OF INVENTION: NOVEL G PROTEINS, POLYNUCLEOTIDE ENCODING THE SAME AND UTILIZATION
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/618,320A
; PRIOR FILING DATE: 2003-07-11
; PRIOR APPLICATION NUMBER: JP 2002/206841
; PRIOR FILING DATE: 2002-07-16
; PRIOR APPLICATION NUMBER: JP 2002/367778
; PRIOR FILING DATE: 2002-12-19
; PRIOR APPLICATION NUMBER: JP 2003/095955
; PRIOR FILING DATE: 2003-03-31
; NUMBER OF SEQ ID NOS: 34
; SEQ ID NO 1:
; LENGTH: 458
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-618-320A-1

Query Match	100.0%	Score	2400	DB	6	Length	458
Best Local Similarity	100.0%	Pred. No.	1.4e-170				
Matches	458	Conservative	0	Mismatches	0	Indels	0
Gaps	0						
QY	1	MGLCYSLRLLFGCGDDPCAA	SEPPVEDAQPAPALAPVRAAARDTARTILPRGEGS	60			
DB	1	MGLCYSLRLLFGCGDDPCAA	SEPPVEDAQPAPALAPVRAAARDTARTILPRGEGS	60			
QY	61	PACARPKADKPKRKRTQLSA	EERAKERAEKVKSGIDRMRLDQRDLQOOTH	120			
DB	61	PACARPKADKPKRKRTQLSA	EERAKERAEKVKSGIDRMRLDQRDLQOOTH	120			
QY	121	RLLLGAGSGKSTIVKQMRIL	HVNGFNPEEKQKILDIRKNVKDAIVTIVSAMSTIPP	180			
DB	121	RLLLGAGSGKSTIVKQMRIL	HVNGFNPEEKQKILDIRKNVKDAIVTIVSAMSTIPP	180			
QY	181	VPLANPENFRSDYIKSIAPIT	DFEYSQBFHVKLWDDEGVKACFERSNEVLIDCAQ	240			
DB	181	VPLANPENFRSDYIKSIAPIT	DFEYSQBFHVKLWDDEGVKACFERSNEVLIDCAQ	240			
QY	241	YFLERIDSVSLVDYTTPTDQ	DLRCRVLTGSGIFRFDVKVNFHMFVGGQRRERKWIQ	300			
DB	241	YFLERIDSVSLVDYTTPTDQ	DLRCRVLTGSGIFRFDVKVNFHMFVGGQRRERKWIQ	300			
QY	301	CFNDVTATIIYAAACSSYNM	VIREDNNTNRLRESLDLFEISWNNRNLRTISILFLNKQDM	360			

301	CFNDVTAIITYAACSSYNKVI	RENDNTNRLRESLDLFESI	WNNRNLRTTISILFLNQDM	360
Db				
361	LAELVLAGSKIEDYFP	PYANTYVPEDATPDAGBD	PKVTRAKFFIRDLFLR	STATGCGK 420
Qy				
361	LAELVLAGSKIEDYFP	PYANTYVPEDATPDAGBD	PKVTRAKFFIRDLFLR	STATGCGK 420
Db				
421	HYCPHFTCAVDTENIR	RVFNDCRDIIQRMHL	KOYELL	458
Qy				
421	HYCPHFTCAVDTENIR	RVFNDCRDIIQRMHL	KOYELL	458
Db				

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RESULT 2
US-10-618-320A-25
; Sequence 25, Application US/10618320A
; Publication No. US20050260595A1
; GENERAL INFORMATION:
; APPLICANT: Sumitomo Chemical Company Limited
; FILE OF INVENTION: NOVEL G PROTEINS, POLYNUCLEOTIDE ENCODING THE SAME AND UTILIZATION THEREOF
; TITLE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/618,320A
; CURRENT FILING DATE: 2003-07-11
; PRIOR APPLICATION NUMBER: JP 2002/206841
; PRIOR FILING DATE: 2002-07-16
; PRIOR APPLICATION NUMBER: JP 2002/367778
; PRIOR FILING DATE: 2002-12-19
; PRIOR APPLICATION NUMBER: JP 2003/095955
; PRIOR FILING DATE: 2003-03-31
; NUMBER OF SEQ ID NOS: 34
; SEQ ID NO 25
; LENGTH: 448
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-618-320A-25

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RESULT 3

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; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 58
; LENGTH: 864
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Synthetic Construct
; NAME/KEY: MISC_FEATURE
; LOCATION: (1)..(864)
; OTHER INFORMATION: pET15b-SD3-ELP1-90-throm-G protein alpha S
US-11-053-100-58

Query Match          64.1%; Score 1538; DB 7; Length 864;
Best Local Similarity 70.8%; Pred. No. 2.4e-106;
Matches 289; Conservative 47; Mismatches 56; Indels 16; Gaps 2;

QY 52 LLPRGEGSPACARPKADPKPKRQTEQLSAREERAAKEREAVKEARKVSRGIDRMLRD 111
DB 472 LVPRGSHMPMALEMGCLGNSKTDQRNEE-----KAQREANKKIEKQLOK 516

QY 112 QKRDLOQTHRLLLGAGESGKSTIVKQMRILHVNENPE-EKKQKILDIRKNVKAIVTI 170
DB 517 DKQVYRATHRLLLGAGESGKSTIVKQMRILHVNENPESEKATKQDINKNLKEAETI 576

QY 171 VSMSTIIPVPLANPENFRSDYIKSIAPITDFEYSQBFDDHVKKLWDDGKACFERS 230
DB 577 VAAMSNLVPVELANPENFRVDYILSVNVPDFPFPFYEHAHALWEDEGVRACYS 636

QY 231 NEVQLDCAQYFLERIDSLVDYTTDQDLRCRVLTSGIFETRFQVDKVNFMHFDVGG 290
DB 637 NEVQLDCAQYFLDKIDVKAQADYVPSDQDLRCRVLTSGIFETRFQVDKVNFMHFDVGG 696

QY 291 QDERERKWKQCFNDVTAIIYVAACSSVMVIREDDNNTNRLRESLDLFSIWNRRWLRTIS 350
DB 697 QDERERKWKQCFNDVTAIIYVASSSYNMVIREDDNNTNRLRESLDLFSIWNRRWLRTIS 756

QY 351 IILFLNKQDLAEKVLAKGSKIEDYFPEYANYTVPEADPDAGEDPKVTRAKFFIRDLFL 410
DB 757 VILFLNKQDLAEKVLAKGSKIEDYFPEYANYTVPEADPDAGEDPKVTRAKFFIRDLFL 816

QY 411 RISTATGDKGHYCPHFTCAVDNTENRRVFNDCRDIIOHMLKQYELL 458
DB 817 RISTASGDRGHYCPHFTCAVDNTENRRVFNDCRDIIOHMLKQYELL 864

RESULT 5
US-10-821-234-1626
; Sequence 1626, Application US/10821234
; Publication No. US20050255114A1
; GENERAL INFORMATION:
; APPLICANT: Labat, Ivan
; APPLICANT: Stache-Crain, Birgit
; APPLICANT: Andarmani, Susan
; APPLICANT: Tang, Y. Tom
; TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
; FILE REFERENCE: 821A
; CURRENT APPLICATION NUMBER: US/10/821,234
; PRIOR FILING DATE: 2004-04-07
; PRIOR FILING DATE: 2003-04-07
; NUMBER OF SEQ ID NOS: 1704
; SOFTWARE: pt_SEQ_genes Version 1.0
; SEQ ID NO 1626
; LENGTH: 394
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-821-234-1626

Query Match          53.6%; Score 1525.5; DB 6; Length 394;
Best Local Similarity 73.8%; Pred. No. 7.4e-106;
Matches 282; Conservative 44; Mismatches 42; Indels 15; Gaps 1;

; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 58
; LENGTH: 864
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Synthetic Construct
; NAME/KEY: MISC_FEATURE
; LOCATION: (1)..(864)
; OTHER INFORMATION: pET15b-SD3-ELP1-90-throm-G protein alpha S
US-11-053-100-58

Query Match          64.1%; Score 1538; DB 7; Length 864;
Best Local Similarity 70.8%; Pred. No. 2.4e-106;
Matches 289; Conservative 47; Mismatches 56; Indels 16; Gaps 2;

QY 52 LLPRGEGSPACARPKADPKPKRQTEQLSAREERAAKEREAVKEARKVSRGIDRMLRD 111
DB 472 LVPRGSHMPMALEMGCLGNSKTDQRNEE-----KAQREANKKIEKQLOK 516

QY 112 QKRDLOQTHRLLLGAGESGKSTIVKQMRILHVNENPE-EKKQKILDIRKNVKAIVTI 170
DB 517 DKQVYRATHRLLLGAGESGKSTIVKQMRILHVNENPESEKATKQDINKNLKEAETI 576

QY 171 VSMSTIIPVPLANPENFRSDYIKSIAPITDFEYSQBFDDHVKKLWDDGKACFERS 230
DB 577 VAAMSNLVPVELANPENFRVDYILSVNVPDFPFPFYEHAHALWEDEGVRACYS 636

QY 231 NEVQLDCAQYFLERIDSLVDYTTDQDLRCRVLTSGIFETRFQVDKVNFMHFDVGG 290
DB 637 NEVQLDCAQYFLDKIDVKAQADYVPSDQDLRCRVLTSGIFETRFQVDKVNFMHFDVGG 696

QY 291 QDERERKWKQCFNDVTAIIYVAACSSVMVIREDDNNTNRLRESLDLFSIWNRRWLRTIS 350
DB 697 QDERERKWKQCFNDVTAIIYVASSSYNMVIREDDNNTNRLRESLDLFSIWNRRWLRTIS 756

QY 351 IILFLNKQDLAEKVLAKGSKIEDYFPEYANYTVPEADPDAGEDPKVTRAKFFIRDLFL 410
DB 757 VILFLNKQDLAEKVLAKGSKIEDYFPEYANYTVPEADPDAGEDPKVTRAKFFIRDLFL 816

QY 411 RISTATGDKGHYCPHFTCAVDNTENRRVFNDCRDIIOHMLKQYELL 458
DB 817 RISTASGDRGHYCPHFTCAVDNTENRRVFNDCRDIIOHMLKQYELL 864

RESULT 6
US-11-060-023-4
; Sequence 4, Application US/11060023
; Publication No. US2005025531A1
; GENERAL INFORMATION:
; APPLICANT: Aventis Pharma Deutschland GmbH
; TITLE OF INVENTION: Process for identifying modulators of G protein coupled
; TITLE OF INVENTION: receptors
; FILE REFERENCE: AVE D-2000/A033 english
; CURRENT APPLICATION NUMBER: US/11/060,023
; CURRENT FILING DATE: 2005-02-17
; PRIOR APPLICATION NUMBER: US/09/899,295
; PRIOR FILING DATE: 2003-07-06
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 353
; TYPE: PRT
; ORGANISM: Mus musculus
US-11-060-023-4

Query Match          30.4%; Score 728.5; DB 7; Length 353;
Best Local Similarity 41.3%; Pred. No. 7.5e-47;
Matches 151; Conservative 69; Mismatches 127; Indels 19; Gaps 4;

QY 93 EAVKEARKVSRGIDRMLRDQKRDLOQTHRLLLGAGESGKSTIVKQMRILHVNENPEEK 152
DB 7 EBAKEARRINDEIERHVRHVRKRDARRELKLLLTGCGSKSTFIKQMRIHSGSYDEDK 66

QY 153 KOKILDIRKNVKAIVTIIVSAMSTIIPVPLANPENQFRSDYIKSTAPITDFEYSQBFDD 212
DB 67 RGFTKLVYQNIPTAMQAMIRAMDTL--KIPYKHNKAHAQLVREDDVEKVSAPENPYVD 124

QY 213 HVKKLWDDGKACFERSNEYQLDCAQYFLERIDSLVDYTTDQDLRCRVLTSGIF 272
DB 125 AIKSLWDDGIGECYDRRREYQLSSTKTYLNDLRVADPAYLPTQDQDLVRVPTGII 184

QY 273 ETRFQVDKVNFMHFDVGGQDERRRKWKQCFNDVTAIIYVAACSSVMVIREDDNNTNRLRE 332
DB 185 EYFPDLQSVIFRMVDVGGQDERRRKWKQCFNDVTAIIYVAACSSVMVIREDDNNTNRLRE 244

QY 333 SLDLPESINWNRWLRTISILFLNKQDLAEKVLAKGSKIEDYFPEYANYTVPEADTPDA 392
DB 185 EYFPDLQSVIFRMVDVGGQDERRRKWKQCFNDVTAIIYVAACSSVMVIREDDNNTNRLRE 244
```

Db 245 SKALFRTIITYPWFQSSVILFLNKKDLLEEKIM--YSHLVDFPEY-----D 290
QY 393 GEDPKVTRAKFFIRDLFLAISTATGKGHCYCPHFTCAVDTENIRRVNDCRDIORMHL 452
Db 291 GPORDAQAAREFLKMFVDLNP---DSDKIYSHFTCATDTENIRVFAAVKDTILQLNL 347
QY 453 KQYELL 458
Db 348 KQYELL 353

RESULT 7
US-11-060-023-8
; Sequence 8, Application US/11060023
; Publication No. US20050255531A1
; GENERAL INFORMATION:
; APPLICANT: Aventis Pharma Deutschland GmbH
; TITLE OF INVENTION: Process for identifying modulators of G protein coupled
; FILE REFERENCE: AVE D-2000/A033 englisch
; CURRENT APPLICATION NUMBER: US/11/060,023
; CURRENT FILING DATE: 2005-02-17
; PRIOR APPLICATION NUMBER: US/09/899,295
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 8
; LENGTH: 353
; TYPE: PRT
; ORGANISM: Mus musculus
US-11-060-023-8

Query Match 30.4%; Score 728.5; DB 7; Length 353;
Best Local Similarity 41.3%; Pred. No. 7.5e-47;
Matches 151; Conservative 69; Mismatches 127; Indels 19; Gaps 4;

QY 93 EAVKEARKVSRGIDRMRLDQKRDLOQTHRLLLLGAGESGKSTIVKOMRILVHNGFNPREK 152
Db 7 EAKEARRINDEIERVRRDKRDARRELKLLLTGSGSKSTFIKQMRIHSGYSDEDK 66

QY 153 KOKILDIRKNVDAIYTVISAMSTIIPPVPLANPENQFRSDYKSIAPITDFEYSQEFDP 212
Db 67 RGFTKLAVYQNIPTAMQAMIRAMDTL--KIPYKYEHNKAHAQLVREVDVKVSAPENPYVD 124

QY 213 HVKKLWDDGKVCACFRSEYQLIDCAQYFLERIDSVSLVDTPTDQDLLRCRVLTSGIF 272
Db 125 AIKSLWNDFGIQECYDRREYQLSDSTKYLNLDLDRVADPAYLPTQDDVLRVVRPTTGI 184

QY 273 ETRFOVDKYNFMDFVGQDERRKWIQCFNDVTAIYVAAACSSYNNMIREDNNTNRLRE 332
Db 185 EYFPDLQSVIFRMVDVGGQSRERKWIHCFNVTSIMFLVALSEYDQVLVESDNENRME 244

QY 333 SLDPESINNRWLRTISILFLNKQDMLAEKVLGAKSKIYDFPEYANYTVPEDATPDA 392
Db 245 SKALFRTIITYPWFQSSVILFLNKKDLLEEKIM--YSHLVDFPEY-----D 290

QY 393 GEDPKVTRAKFFIRDLFLAISTATGKGHCYCPHFTCAVDTENIRRVNDCRDIORMHL 452
Db 291 GPORDAQAAREFLKMFVDLNP---DSDKIYSHFTCATDTENIRVFAAVKDTILQLNL 347

QY 453 KQYELL 458
Db 348 KQYELL 353

RESULT 8
US-11-053-100-52
; Sequence 52, Application US/11053100
; Publication No. US20050255534A1
; GENERAL INFORMATION:
; APPLICANT: CHILKOTI, Ashutosh
; TITLE OF INVENTION: FUSION PEPTIDES ISOLATABLE BY PHASE TRANSITION
; FILE REFERENCE: 4176-101 CIP

; CURRENT APPLICATION NUMBER: US/11/053,100
; CURRENT FILING DATE: 2005-02-08
; PRIOR APPLICATION NUMBER: US 09/812,382
; PRIOR FILING DATE: 2001-03-20
; PRIOR APPLICATION NUMBER: US 60/190,659
; PRIOR FILING DATE: 2000-03-20
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 52
; LENGTH: 859
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Synthetic Construct
; FEATURE:
; NAME/KEY: MISC_FEATURE
; LOCATION: (1)..(859)
; OTHER INFORMATION: pET15b-SD1-ELP1-90-throm-G protein alpha Q
US-11-053-100-52

Query Match 30.1%; Score 723.5; DB 7; Length 859;
Best Local Similarity 38.6%; Pred. No. 5.5e-46;
Matches 158; Conservative 76; Mismatches 154; Indels 21; Gaps 5;

QY 52 LLPRGEGSPACARPKADPK--EKQRTEQLSAEEREAAKEREAVKEARKVSRGIDRML 109
Db 470 LVPRGSHMGLNDIFEAQKIEWHEHMPMALENTLSEINACCLSEAKEARRINDEIERQL 529

QY 110 RDQKRDLOQTHRLLLLGAGESGKSTIVKOMRILVHNGFNPEKKOKILDIRKNVDAIYTV 169
Db 530 RDKKRDARRELKLLLTGSGSKSTFIKQMRIHSGYSDEDKRGFTKLAVYQNIPTAMQA 589

QY 170 IVSAMSTIIPPVPLANPENQFRSDYKSIAPITDFEYSQEFDPDHVKKLWDDGKVCACFR 229
Db 590 MIRAMDTL--KIPYKYEHNKAHAQLVREVDVKVSAPENPYVDIAIKSLWNDFGIQECYDR 647

QY 230 SNEYQLIDCAQYFLERIDSVSLVDTPTDQDLLRCRVLTSGIFETRFQVDKYNFMDFVG 289
Db 648 RREYQLSDSTKYLNLDLDRVADPAYLPTQDDVLRVVRPTTGIIEYFPDLQSVIFRMVDVG 707

QY 290 GQDERRKWIQCFNDVTAIYVAAACSSYNNMIREDNNTNRLRESLDLPESINNRWLRTI 349
Db 708 QQRSEKRWIHCFNVTSIMFLVALSEYDQVLVESDNENRMEESKALFRTIITYPWFQNS 767

QY 350 SIILFLNKQDMLAEKVLGAKSKIYDFPEYANYTVPEDATPDAEDPKVTRAKFFIRDLF 409
Db 768 SVILFLNKKDLLEEKIM--YSHLVDFPEY-----DGPORDAQAAREFLKMF 813

QY 410 LRISTATGKGHCYCPHFTCAVDTENIRRVNDCRDIORMHLKQYELL 458
Db 814 VDLNP---DSDKINYSHFTCATDTENIRVFAAVKDTILQLNLKEYNLV 859

RESULT 9
US-11-053-100-53
; Sequence 53, Application US/11053100
; Publication No. US20050255534A1
; GENERAL INFORMATION:
; APPLICANT: CHILKOTI, Ashutosh
; TITLE OF INVENTION: FUSION PEPTIDES ISOLATABLE BY PHASE TRANSITION
; FILE REFERENCE: 4176-101 CIP
; CURRENT APPLICATION NUMBER: US/11/053,100
; CURRENT FILING DATE: 2005-02-08
; PRIOR APPLICATION NUMBER: US 09/812,382
; PRIOR FILING DATE: 2001-03-20
; PRIOR APPLICATION NUMBER: US 60/190,659
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 53
; LENGTH: 1309
; TYPE: PRT
; ORGANISM: Artificial


```
Db 342 AAVKDTILQLNLKEYNLV 359
; LENGTH: 353
; TYPE: PRT
; ORGANISM: Mus musculus
US-11-060-023-14

RESULT 12
US-11-060-023-12
; Sequence 12, Application US/11060023
; Publication No. US2005025531A1
; GENERAL INFORMATION:
; APPLICANT: Aventis Pharma Deutschland GmbH
; TITLE OF INVENTION: Process for identifying modulators of G protein coupled
; TITLE OF INVENTION: receptors
; FILE REFERENCE: AVE D-2000/A033 englisch
; CURRENT APPLICATION NUMBER: US/11/060,023
; PRIOR FILING DATE: 2005-02-17
; PRIOR APPLICATION NUMBER: US/09/899,295
; PRIOR FILING DATE: 2003-07-06
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 12
; LENGTH: 353
; TYPE: PRT
; ORGANISM: Mus musculus
US-11-060-023-12

Query Match 29.9%; Score 717.5; DB 7; Length 353;
Best Local Similarity 40.4%; Pred. No. 4.9e-46;
Matches 148; Conservative 71; Mismatches 128; Indels 19; Gaps 4;

QY 93 EAVKEARKVSRGIDRMRLDQKRDLOQTHRLLLGAGESGKSTIVKQMRILHVNQFNPEEK 152
DB 7 EEAKARRINDEIERHVRDRKRDARRELKLLLTGSGSKSTFIKQMRIHSGYSDEK 66
QY 153 KQKILDIRKNVKDAIVTIVSAMSTIIPVPLANPENQFRSDYIKSTAPITDFYSQEFFD 212
DB 67 RGFTKLVYQNIPTAMQAMIRAMDTL--KIPYKYEHNKAHAQLVREVDVEKVSAPENPYVD 124
QY 213 HVKKLWDEGVKACFERSNEYQLIDCAQYFLERIDSVLSVDYPTDQDLRCRVLTSGIF 272
DB 125 AIKSLWDPGIEQCYDRRRYQLSDTKYVNLNDRVADPAYLPTQDVLVRVPTGII 184
QY 273 ETRFQVDKVNFMHFDVGQDRERRKWTQCFNDVTAIIVAACSSYNMVIREDNNTNRLRE 332
DB 185 EYPFDLQSVIFRMVDVGQSRERRKWIHCENVTSMFLVALSEYDQVLVESDNRMEE 244
QY 333 SLDLFESINNRWLRTSIILFLNKQDMLAEKVLGSKIEDYFPEYANVTVPEDATPDA 392
DB 245 SKALFRTIITYPWFQNSSVILFLNKKDLLEKIM--YSHLVDFPEY-----D 290
QY 393 GEDPKVTRAKFFIRDLFLRISTATGDKGHYCYPHFTCAVDTENIRRVFNDCRDIIQRMHL 452
DB 291 GPORDAQAREFILKMFVDLNP---DSDKIYSHFTCATDTENIRFVFAAVKDTILQLNL 347
QY 453 QYELL 458
DB 348 KEYNLV 353

RESULT 13
US-11-060-023-14
; Sequence 14, Application US/11060023
; Publication No. US2005025531A1
; GENERAL INFORMATION:
; APPLICANT: Aventis Pharma Deutschland GmbH
; TITLE OF INVENTION: Process for identifying modulators of G protein coupled
; TITLE OF INVENTION: receptors
; FILE REFERENCE: AVE D-2000/A033 englisch
; CURRENT APPLICATION NUMBER: US/11/060,023
; PRIOR FILING DATE: 2005-02-17
; PRIOR APPLICATION NUMBER: US/09/899,295
; PRIOR FILING DATE: 2003-07-06
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 14

Query Match 29.9%; Score 717.5; DB 7; Length 359;
Best Local Similarity 40.4%; Pred. No. 5e-46;
Matches 148; Conservative 71; Mismatches 128; Indels 19; Gaps 4;

QY 93 EAVKEARKVSRGIDRMRLDQKRDLOQTHRLLLGAGESGKSTIVKQMRILHVNQFNPEEK 152
DB 13 EEAKARRINDEIERHVRDRKRDARRELKLLLTGSGSKSTFIKQMRIHSGYSDEK 72
QY 153 KQKILDIRKNVKDAIVTIVSAMSTIIPVPLANPENQFRSDYIKSTAPITDFYSQEFFD 212
DB 73 RGFTKLVYQNIPTAMQAMIRAMDTL--KIPYKYEHNKAHAQLVREVDVEKVSAPENPYVD 130
QY 213 HVKKLWDEGVKACFERSNEYQLIDCAQYFLERIDSVLSVDYPTDQDLRCRVLTSGIF 272
; SEQ ID NO 14
```

Db 131 AIKSLWMDPGIQECYDRRREYQLSDSTKYVINDLDRVADPAYLPQQDVLVRVPTTGII 190
Qy 273 ETRFQVDKYNHMFVDCGQDERRKWIQCFNDVTAIYVAAACSSYNMVIREDNNNTNRLRE 332
Db 191 EYPFDLQSVIFRMVDVGQSRERKWIHCFENVTSIMFLVALSEYDQVLVESDNERMEE 250
Qy 333 SLDLFESIMNRLRTISILFLNKQDMLAEKVLGKSKIEDYPEYANVTVPEDATPDA 392
Db 251 SKALFRITIIYFPWFQNSVILFLNKKDLEEKIM--YSHLVDYPPPEY-----D 296
Qy 393 GEDPKVTRAKFFIRDLFLRISTATGDKGHYCYPHFTCAVDTENIRRVFNDCRDIIQRMHL 452
Db 297 GPORDAQAAREFILKMFVDLNP---DSDKIIYSHFTCATDTENIRFVFAAVKDTILQLNL 353
Qy 453 KQYELL 458
Db 354 KEYNLV 359

RESULT 15

US-11-060-023-17
; Sequence 17, Application US/11060023
; Publication No. US2005025531A1
; GENERAL INFORMATION:
; APPLICANT: Aventis Pharma Deutschland GmbH
; TITLE OF INVENTION: Process for identifying modulators of G protein coupled
; TITLE OF INVENTION: receptors
; FILE REFERENCE: AVE D-2000/A033 englisch
; CURRENT APPLICATION NUMBER: US/11/060,023
; CURRENT FILING DATE: 2005-02-17
; PRIOR APPLICATION NUMBER: US/09/899,295
; PRIOR FILING DATE: 2003-07-06
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 17
; LENGTH: 360
; TYPE: PRT
; ORGANISM: Mus musculus
US-11-060-023-17

Query Match 29.9%; Score 717.5; DB 7; Length 360;
Best Local Similarity 40.2%; Pred. No. 5e-46;
Matches 148; Conservative 72; Mismatches 129; Indels 19; Gaps 4;
Qy 91 EREAVKEARKVSRGIDRMLRDKRDQLQOQTHRLLLGAGESGKSTIVKQMRILHVGNFPE 150
Db 12 QRNEEKEARRINDEIERHVRDRDKDARRELKLLLLGTGESGKSTFIKQMRIHSGYSDE 71
Qy 151 EKQKILDIRNVKDAIVTVISAMSTIIPVPLANPENQPRSDYIKSIAPITDFEYSQEF 210
Db 72 DKGFTKLVYQNIPTAQMAMIRAMDTL--KIPYKYEHNKAHAQLVREVDVEKVSFAFENPY 129
Qy 211 FDHVKKLWDDGKACFERSNEYOLIDCAQYFLERIDSVLSVDYPTDQDLRLCRVLTS 270
Db 130 VDAIKSLWNDPGIOECYDRRREYQLSDSTKYVINDLDRVADPAYLPQQDVLVRVPTTG 189
Qy 271 IFETRFQVDKYNHMFVDCGQDERRKWIQCFNDVTAIYVAAACSSYNMVIREDNNNTNRL 330
Db 190 IIEYFPDLQSVIFRMVDVGQSRERKWIHCFENVTSIMFLVALSEYDQVLVESDNERM 249
Qy 331 RESLDLPESIMNRLRTISILFLNKQDMLAEKVLGKSKIEDYPEYANVTVPEDATP 390
Db 250 EESKALFRITIIYFPWFQNSVILFLNKKDLEEKIM--YSHLVDYPPPEY----- 296
Qy 393 DAGEDPKVTRAKFFIRDLFLRISTATGDKGHYCYPHFTCAVDTENIRRVFNDCRDIIQRM 450
Db 297 -DGPORDAQAAREFILKMFVDLNP---DSDKIIYSHFTCATDTENIRFVFAAVKDTILQL 352
Qy 451 HLKQYELL 458
Db 353 NLKEYNLV 360

Search completed: March 2, 2006, 19:38:17
Job time : 16.9223 secs

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OM protein - protein search, using sw model

Run on: March. 2, 2006, 19:29:36 ; Search time 9.63599 Seconds
(without alignments)
1413.528 Million cell updates/sec

Title: US-10-618-320A-1_COPY_96_126
Perfect score: 153
Sequence: 1 KEARKVSRGIDRLMDQKRLDQTHRLLLG 31

Scoring table: BLOSUM62

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_21.*
1: Geneseqp1980s.*
2: Geneseqp1990s.*
3: Geneseqp2000s.*
4: Geneseqp2001s.*
5: Geneseqp2002s.*
6: Geneseqp2003s.*
7: Geneseqp2003bs.*
8: Geneseqp2004s.*
9: Geneseqp2005s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	153	100.0	150	9	AEAL7334
2	153	100.0	202	9	AEAL7301
3	153	100.0	458	8	ADG74722 Human G-p
4	153	100.0	458	9	AEAL7292
5	153	100.0	461	4	ABG01236
6	149	97.4	230	9	AEAL7296
7	149	97.4	448	8	ADG74746
8	149	97.4	450	8	ADG74747
9	79	51.6	385	8	ADN2325 Bacterial
10	76	49.7	353	4	ABG9072 Human G-p
11	76	49.7	353	5	ABG68587
12	76	49.7	353	5	ABG68585
13	76	49.7	353	5	ABG68599
14	76	49.7	353	5	ABG09281
15	76	49.7	353	7	ABR82631 C. elegans
16	76	49.7	353	7	ADC09616 Human G-p
17	76	49.7	353	8	ADS73825
18	76	49.7	353	8	ADU60735
19	76	49.7	353	9	ADY64330 Mouse G-p
20	76	49.7	359	2	AAAY49125
21	76	49.7	359	5	ABG68598
22	76	49.7	359	5	ABG68603
23	76	49.7	359	5	ABG68586
24	76	49.7	359	5	ABG68584

RESULT 1
AEAL7334
ID AEAL7334 standard; protein; 150 AA.
XX AC AEAL7334;
XX XX
DT 28-JUL-2005 (first entry)
XX XX
DE N-terminal human XLG(olf) protein fragment Seq 44.
XX XLG(olf); G protein coupled receptor; schizophrenia;
KW psychiatric disorder; neuroleptic; gene therapy.
KW psychiatric disorder; neuroleptic; gene therapy.
XX Homo sapiens.
XX XX
PN WO2005047318-A1.
XX XX
PD 26-MAY-2005.
XX XX
PF 11-NOV-2004; 2004WO-GB004749.
XX XX
PR 11-NOV-2003; 2003US-0519190P.
PR 03-SEP-2004; 2004US-0607010P.
XX (ASTR) ASTRAZENECA AB.
XX (ASTR) ASTRAZENECA UK LTD.
PI Bostwick RJ, Corradi J, Defay T, Furlong S, Hirata LT, Ravyn V;
PI Robbins A;
XX WPI; 2005-386333/39.
XX New isolated nucleic acid molecule encoding Golf G proteins, useful for
PT identifying modulators of G protein coupled receptor activity, or for
PT diagnosing or treating schizophrenia and other psychiatric disorders.
PS Disclosure; SEQ ID NO 44; 235pp; English.
XX This invention relates to a novel transcriptional variant of the human
CC GNAL gene that encodes a novel splice variant of the G protein alpha
CC subunit protein Golf, referred to herein as XLGolf, as well as methods
CC for identifying modulators of G protein coupled receptors (GPCRs). Note
CC that the N-terminus of the XLGolf protein is altered compared to Golf
CC with a different exon 1. Specifically, it refers to contacting the GPCR
CC with a test compound, and determining GPCR activity, where a change in
CC activity indicates that the compound is a modulator thereof. The present
CC invention describes the GPCR as a Gs coupled GPCR that is selected from

ALIGNMENTS

25	76	49.7	359	5	ABG68593	Abg68593 Mouse G p
26	76	49.7	359	5	ABG68610	Abg68610 Human G p
27	76	49.7	359	7	ADP70780	Adp70780 Minicell
28	76	49.7	359	8	ADN06136	Adn06136 Human Gq
29	76	49.7	359	9	ADX07219	Adx07219 Cyclin-de
30	76	49.7	359	9	ABE71353	AbE71353 Human mod
31	76	49.7	360	8	ADN06150	Adn06150 Rat Gii-H
32	76	49.7	360	8	ADN06148	Adn06148 Rat Gii-H
33	76	49.7	499	9	ADY14842	Ady14842 PRO polyP
34	76	49.7	1276	2	AAAY49127	AAy49127 phCaR/hmG
35	76	49.7	1276	5	AAOI5093	AAo15093 Human phC
36	76	49.7	1303	2	AAAY49132	AAy49132 GABA-BR2*
37	76	49.7	1303	5	AAOI5098	AAo15098 Human GAB
38	76	49.7	1323	2	AAAY49133	AAy49133 GABA-BR1a
39	76	49.7	1323	5	AAOI5099	AAo15099 Human GAB
40	76	49.7	1394	2	AAAY49129	AAy49129 pmGluR2/C
41	76	49.7	1394	5	AAOI5095	AAo15095 Human pmG
42	76	49.7	1397	2	AAAY49134	AAy49134 pmGluR2/C
43	76	49.7	1397	5	AAOI5100	AAo15100 Human pmG
44	76	49.7	1402	5	AAOI5105	AAo15105 Human ph2
45	76	49.7	1418	2	AAAY49131	AAy49131 mGluR8/Ca

CC dopamine receptor D1, adenosine A2a receptor, and adrenergic beta-2
 CC receptor. Accordingly, the composition and methods are useful for
 CC identifying modulators of GPCR activity, as well as for diagnosing or
 CC treating schizophrenia and other psychiatric disorders. Furthermore, the
 CC pharmaceutical compositions derived thereof exhibit neuroleptic activity
 CC and can be used for gene therapy purposes. This polypeptide sequence is
 CC an N-terminal fragment of the human XLG(olf) protein of the invention.

XX
 SQ Sequence 150 AA;

Query Match 100.0%; Score 153; DB 9; Length 150;
 Best Local Similarity 100.0%; Pred. No. 3.8e-13;
 Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KEARKVSRGIDRMRLDKRDQLQOQTHRLLLG 31
 |||||
 DB 96 KEARKVSRGIDRMRLDKRDQLQOQTHRLLLG 126

RESULT 2

ID AEA17301 standard; protein; 202 AA.

XX AEA17301;

AC AEA17301;

XX 28-JUL-2005 (first entry)

DT Human XLGalphas protein fragment (encoded by alternate transcript) Seq11.

DE Human XLGalphas; G protein coupled receptor; schizophrenia;
 KW psychiatric disorder; neuroleptic; gene therapy.

XX Homo sapiens.

OS WO2005047318-A1.

PN 26-MAY-2005.

XX 11-NOV-2004; 2004WO-GB004749.

XX 11-NOV-2003; 2003US-0519190P.

PR 03-SEP-2004; 2004US-0607010P.

XX (ASTR) ASTRAZENECA AB.

PA (ASTR) ASTRAZENECA UK LTD.

XX Boetwick RJ, Corradi J, Defay T, Furlong S, Hirata LT, Ravyn V;
 PI Robbins A;

XX WPI; 2005-386333/39.

XX New isolated nucleic acid molecule encoding Golf G proteins, useful for
 PT identifying modulators of G protein coupled receptor activity, or for
 PT diagnosing or treating schizophrenia and other psychiatric disorders.

XX Disclosure; SEQ ID NO 11; 235pp; English.

XX This invention relates to a novel transcriptional variant of the human
 CC GNAL gene that encodes a novel splice variant of the G protein alpha
 CC subunit protein Golf, referred to herein as XLGolf, as well as methods
 CC for identifying modulators of G protein coupled receptors (GPCRs). Note
 CC that the N-terminus of the XLGolf protein is altered compared to Golf
 CC with a different exon 1. Specifically, it refers to contacting the GPCR
 CC with a test compound, and determining GPCR activity, where a change in
 CC activity indicates that the compound is a modulator thereof. The present
 CC invention describes the GPCR as a Gs coupled GPCR that is selected from
 CC dopamine receptor D1, adenosine A2a receptor, and adrenergic beta-2
 CC receptor. Accordingly, the composition and methods are useful for
 CC identifying modulators of GPCR activity, as well as for diagnosing or
 CC treating schizophrenia and other psychiatric disorders. Furthermore, the
 CC pharmaceutical compositions derived thereof exhibit neuroleptic activity
 CC and can be used for gene therapy purposes. This polypeptide sequence is
 CC an N-terminal fragment of the human XLGalphas protein of the invention.

XX
 SQ Sequence 202 AA;

Query Match 100.0%; Score 153; DB 9; Length 202;
 Best Local Similarity 100.0%; Pred. No. 5.2e-13;
 Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KEARKVSRGIDRMRLDKRDQLQOQTHRLLLG 31
 |||||
 DB 96 KEARKVSRGIDRMRLDKRDQLQOQTHRLLLG 126

RESULT 3

ID ADG74722 standard; protein; 458 AA.

XX ADG74722;

AC ADG74722;

XX 22-APR-2004 (first entry)

DT Human G-protein Gml amino acid sequence.

DE Human G-protein; Gml; G protein-coupled receptor mediated signal transduction;
 KW GTP binding site; GTPase site; G protein alpha subunit;
 KW signal transduction; G-protein-coupled receptor.

XX Homo sapiens.

OS EP1382613-A1.

XX 21-JAN-2004.

XX 09-JUL-2003; 2003EP-00015519.

XX 16-JUL-2002; 2002JP-00206841.

PR 19-DEC-2002; 2002JP-00367778.

PR 31-MAR-2003; 2003JP-00095955.

XX (SUMO) SUMITOMO CHEM CO LTD.

XX Takahashi Y, Matsumoto Y, Oeda K;
 PI WPI; 2004-111483/12.

XX N-PSDB; ADG74723.

DR New protein useful as a therapeutic or prophylactic agent against a
 PT disease caused by an abnormality in a G-protein coupled receptor mediated
 PT signal transduction.

XX Claim 1; SEQ ID NO 1; 85pp; English.

XX This invention relates to a novel G protein (Gml). The protein is
 CC involved in a G protein-coupled receptor mediated signal transduction.
 CC The protein of the invention has a sequence with a high homology with a
 CC GTP binding site and a GTPase site conserved among G protein alpha
 CC subunits. The protein, the DNA sequence which encodes it and an antibody
 CC specifically recognizing the protein of the invention may be useful as a
 CC therapeutic or prophylactic agent against a disease caused by an
 CC abnormality in a G-protein coupled receptor mediated signal transduction.
 CC The invention may also be useful for screening for a substance capable of
 CC regulating a signal transduction mediated by a G-protein-coupled receptor
 CC and a protein.

XX Sequence 458 AA;

Query Match 100.0%; Score 153; DB 8; Length 458;
 Best Local Similarity 100.0%; Pred. No. 1.2e-12;
 Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KEARKVSRGIDRMRLDKRDQLQOQTHRLLLG 31
 |||||
 DB 96 KEARKVSRGIDRMRLDKRDQLQOQTHRLLLG 126

RESULT 4
 AEA17292
 ID AEA17292 standard; protein; 458 AA.
 XX AC AEA17292;
 XX DT 28-JUL-2005 (first entry)
 XX DE Human XLGolf protein Seq 2.
 XX KW XLGolf; G protein coupled receptor; schizophrenia; psychiatric disorder;
 XX KW neuroleptic; gene therapy.
 XX OS Homo sapiens.
 XX PN WO2005047318-A1.
 XX PD 26-MAY-2005.
 XX PF 11-NOV-2004; 2004WO-GB004749.
 XX PR 11-NOV-2003; 2003US-0519190P.
 XX PR 03-SEP-2004; 2004US-0607010P.
 XX PA (ASTR) ASTRAZENECA AB.
 XX PA (ASTR) ASTRAZENECA UK LTD.
 XX PI Bostwick RJ, Corradi J, Defay T, Furlong S, Hirata LT, Ravyn V;
 XX PI Robbins A;
 XX PS WPI; 2005-386333/39.
 XX DR N-PSDB; AEA17291, AEA17302.
 XX PT New isolated nucleic acid molecule encoding Golf G proteins, useful for
 PT identifying modulators of G protein coupled receptor activity, or for
 PT diagnosing or treating schizophrenia and other psychiatric disorders.
 XX Claim 8; SEQ ID NO 2; 235pp; English.
 XX CC This invention relates to a novel transcriptional variant of the human
 CC GNAL gene that encodes a novel splice variant of the G protein alpha
 CC subunit protein Golf, referred to herein as XLGolf, as well as methods
 CC for identifying modulators of G protein coupled receptors (GPCRs). Note
 CC that the N-terminus of the XLGolf protein is altered compared to Golf
 CC with a different exon 1. Specifically, it refers to contacting the GPCR
 CC with a test compound, and determining GPCR activity, where a change in
 CC activity indicates that the compound is a modulator thereof. The present
 CC invention describes the GPCR as a Gs coupled GPCR that is selected from
 CC dopamine receptor D1, adenosine A2a receptor, and adrenergic beta-2
 CC receptor. Accordingly, the composition and methods are useful for
 CC identifying modulators of GPCR activity, as well as for diagnosing or
 CC treating schizophrenia and other psychiatric disorders. Furthermore, the
 CC pharmaceutical compositions derived thereof exhibit neuroleptic activity
 CC and can be used for gene therapy purposes. This polypeptide sequence is
 CC the human XLGolf protein of the invention.
 XX SQ Sequence 458 AA;
 Query Match 100.0%; Score 153; DB 9; Length 458;
 Best Local Similarity 100.0%; Pred. No. 1.2e-12;
 Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 KEARKVSRGIDRMRLDKRDLQOQTHRLLLG 31
 |||||
 Db 96 KEARKVSRGIDRMRLDKRDLQOQTHRLLLG 126
 RESULT 5
 ABG01236
 ID ABG01236 standard; protein; 461 AA.
 XX AC ABG01236;

XX 13-FEB-2002 (first entry)
 DT XX Novel human diagnostic protein #1227.
 DE XX Human; chromosome mapping; gene mapping; gene therapy; forensic;
 KW food supplement; medical imaging; diagnostic; genetic disorder.
 KW OS Homo sapiens.
 XX PN WO200175067-A2.
 XX PD 11-OCT-2001.
 XX PF 30-MAR-2001; 2001WO-US008631.
 XX PR 31-MAR-2000; 2000US-00540217.
 XX PR 23-AUG-2000; 2000US-00649167.
 XX PA (HYSE-) HYSEQ INC.
 XX PI Drmanac RT, Liu C, Tang YT;
 XX PI WPI; 2001-639362/73.
 XX DR N-PSDB; AAS65423.
 XX PT New isolated polynucleotide and encoded polypeptides, useful in
 PT diagnostics, forensics, gene mapping, identification of mutations
 PT responsible for genetic disorders or other traits and to assess
 PT biodiversity.
 XX Claim 20; SEQ ID NO 31595; 103pp; English.
 XX CC The invention relates to isolated polynucleotide (I) and polypeptide (II)
 CC sequences. (I) is useful as hybridisation probes, polymerase chain
 CC reaction (PCR) primers, oligomers, and for chromosome and gene mapping,
 CC and in recombinant production of (II). The polynucleotides are also used
 CC in diagnostics as expressed sequence tags for identifying expressed
 CC genes. (I) is useful in gene therapy techniques to restore normal
 CC activity of (II) or to treat disease states involving (II). (II) is
 CC useful for generating antibodies against it, detecting or quantitating a
 CC polypeptide in tissue, as molecular weight markers and as a food
 CC supplement. (II) and its binding partners are useful in medical imaging
 CC of sites expressing (II). (I) and (II) are useful for treating disorders
 CC involving aberrant protein expression or biological activity. The
 CC polypeptide and polynucleotide sequences have applications in
 CC diagnostics, forensics, gene mapping, identification of mutations
 CC responsible for genetic disorders or other traits to assess biodiversity
 CC and to produce other types of data and products dependent on DNA and
 CC amino acid sequences. ABG00010-ABG30377 represent novel human diagnostic
 CC amino acid sequences of the invention. Note: The sequence data for this
 CC patent did not appear in the printed specification, but was obtained in
 CC electronic format directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX SQ Sequence 461 AA;
 Query Match 100.0%; Score 153; DB 4; Length 461;
 Best Local Similarity 100.0%; Pred. No. 1.2e-12;
 Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 KEARKVSRGIDRMRLDKRDLQOQTHRLLLG 31
 |||||
 Db 96 KEARKVSRGIDRMRLDKRDLQOQTHRLLLG 126
 RESULT 6
 AEA17296
 ID AEA17296 standard; protein; 230 AA.
 XX AC AEA17296;
 XX DT 28-JUL-2005 (first entry)

```

XX Murine XLGolf protein Seq 6.
DE
XX
XX XLGolf; G protein coupled receptor; schizophrenia; psychiatric disorder;
KW neuroleptic; gene therapy.
XX
XX Mus musculus.
OS
XX
XX W02005047318-A1.
PN
XX
XX 26-MAY-2005.
PD
XX
XX 11-NOV-2004; 2004WO-GB004749.
PF
XX
XX 11-NOV-2003; 2003US-0519190P.
PR
XX 03-SEP-2004; 2004US-0607010P.
PR
XX
XX (ASTR ) ASTRAZENECA AB.
PA
XX (ASTR ) ASTRAZENECA UK LTD.
PA
XX
XX Bostwick RJ, Corradi J, Defay T, Furlong S, Hirata LT, Ravyn V;
PI Robbins A;
PI
XX
XX WPI; 2005-386333/39.
DR
XX N-PSDB; ABA17295.
DR
XX
XX New isolated nucleic acid molecule encoding Golf G proteins, useful for
PT identifying modulators of G protein coupled receptor activity, or for
PT diagnosing or treating schizophrenia and other psychiatric disorders.
XX
XX Example 1; SEQ ID NO 6; 235pp; English.
PS
XX
XX This invention relates to a novel transcriptional variant of the human
CC GNAL gene that encodes a novel splice variant of the G protein alpha
CC subunit protein Golf, referred to herein as XLGolf, as well as methods
CC for identifying modulators of G protein coupled receptors (GPCRs). Note
CC that the N-terminus of the XLGolf protein is altered compared to Golf
CC with a different exon 1. Specifically, it refers to contacting the GPCR
CC with a test compound, and determining GPCR activity, where a change in
CC activity indicates that the compound is a modulator thereof. The present
CC invention describes the GPCR as a Gs coupled GPCR that is selected from
CC dopamine receptor D1, adenosine A2a receptor, and adrenergic beta-2
CC receptor. Accordingly, the composition and methods are useful for
CC identifying modulators of GPCR activity, as well as for diagnosing or
CC treating schizophrenia and other psychiatric disorders. Furthermore, the
CC pharmaceutical compositions derived thereof exhibit neuroleptic activity
CC and can be used for gene therapy purposes. This polypeptide sequence is
CC the murine XLGolf protein of the invention.
XX
XX Sequence 230 AA;
.SQ
Query Match 97.4%; Score 149; DB 9; Length 230;
Best Local Similarity 96.8%; Pred. No. 2.1e-12;
Matches 30; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 KEARKVSRGIDRLMDQKRDLDQOQTHRLLLG 31
DB 86 KEARKVSRGIDRLMDQKRDLDQOQTHRLLLG 116
RESULT 7
ADG74746
ID ADG74746 standard; protein; 448 AA.
XX
XX ADG74746;
AC
XX
XX 22-APR-2004 (first entry)
DT
XX
XX Mouse G-protein Gml amino acid sequence.
DE
XX
XX G protein; Gml; G protein-coupled receptor mediated signal transduction;
KW GTP binding site; GTPase site; G protein alpha subunit;
KW signal transduction; G-protein-coupled receptor; mouse; murine.
XX

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XX Mus musculus.
OS
XX
XX EP1382613-A1.
PN
XX
XX 21-JAN-2004.
PD
XX
XX 09-JUL-2003; 2003EP-00015519.
PF
XX
XX 16-JUL-2002; 2002JP-00206841.
PR
XX 19-DEC-2002; 2002JP-00367778.
PR
XX 31-MAR-2003; 2003JP-00095955.
PR
XX
XX (SUMO ) SUMITOMO CHEM CO LTD.
PA
XX
XX Takahashi Y, Matsumoto Y, Oeda K;
PI
XX WPI; 2004-111483/12.
DR
XX N-PSDB; ADG74748.
DR
XX
XX New protein useful as a therapeutic or prophylactic agent against a
PT disease caused by an abnormality in a G-protein coupled receptor mediated
PT signal transduction.
XX
XX Claim 1; SEQ ID NO 25; 85pp; English.
PS
XX
XX This invention relates to a novel G protein (Gml). The protein is
CC involved in a G protein-coupled receptor mediated signal transduction.
CC The protein of the invention has a sequence with a high homology with a
CC GTP binding site and a GTPase site conserved among G protein alpha
CC subunits. The protein, the DNA sequence which encodes it and an antibody
CC specifically recognizing the protein of the invention may be useful as a
CC therapeutic or prophylactic agent against a disease caused by an
CC abnormality in a G-protein coupled receptor mediated signal transduction.
CC The invention may also be useful for screening for a substance capable of
CC regulating a signal transduction mediated by a G-protein-coupled receptor
CC and a protein. The present sequence is that of the mouse Gml protein
CC which is related to the human Gml protein of the invention.
XX
XX Sequence 448 AA;
.SQ
Query Match 97.4%; Score 149; DB 8; Length 448;
Best Local Similarity 96.8%; Pred. No. 4.2e-12;
Matches 30; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 KEARKVSRGIDRLMDQKRDLDQOQTHRLLLG 31
DB 86 KEARKVSRGIDRLMDQKRDLDQOQTHRLLLG 116
RESULT 8
ADG74747
ID ADG74747 standard; protein; 450 AA.
XX
XX ADG74747;
AC
XX
XX 22-APR-2004 (first entry)
DT
XX
XX Rat G-protein Gml amino acid sequence.
DE
XX
XX G protein; Gml; G protein-coupled receptor mediated signal transduction;
KW GTP binding site; GTPase site; G protein alpha subunit;
KW signal transduction; G-protein-coupled receptor; rat.
XX
XX Rattus norvegicus.
OS
XX
XX EP1382613-A1.
PN
XX
XX 21-JAN-2004.
PD
XX
XX 09-JUL-2003; 2003EP-00015519.
PF
XX
XX 16-JUL-2002; 2002JP-00206841.
PR

```

PR 19-DEC-2002; 2002JP-00367778.
PR 31-MAR-2003; 2003JP-00095955.
XX (SUMO) SUMITOMO CHEM CO LTD.
XX Takahashi Y, Matsumoto Y, Oeda K;
XX WPI; 2004-111483/12.
DR N-PSDB; ADG74749.
XX
PT New protein useful as a therapeutic or prophylactic agent against a
PT disease caused by an abnormality in a G-protein coupled receptor mediated
PT signal transduction.
XX
PS Claim 1; SEQ ID NO 26; 85pp; English.
XX
CC This invention relates to a novel G protein (Gml). The protein is
CC involved in a G protein-coupled receptor mediated signal transduction.
CC The protein of the invention has a sequence with a high homology with a
CC GTP binding site and a GTPase site conserved among G protein alpha
CC subunits. The protein, the DNA sequence which encodes it and an antibody
CC specifically recognising the protein of the invention may be useful as a
CC therapeutic or prophylactic agent against a disease caused by an
CC abnormality in a G-protein coupled receptor mediated signal transduction.
CC The invention may also be useful for screening for a substance capable of
CC regulating a signal transduction mediated by a G-protein-coupled receptor
CC and a protein. The present sequence is that of the rat Gml protein which
CC is related to the human Gml protein of the invention.
XX
SQ Sequence 450 AA;
Query Match 97.4%; Score 149; DB 8; Length 450;
Best Local Similarity 96.8%; Pred. No. 4.2e-12;
Matches 30; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 KEARKVSRGIDRLMDKRDLDQOQTHRLLLIG 31
Db 88 KEARKVSRGIDRLMDKRDLDQOQTHRLLLIG 118
RESULT 9
ADN22325
ID ADN22325 standard; protein; 385 AA.
XX
AC ADN22325;
XX
DT 02-DEC-2004 (first entry)
XX
DE Bacterial polypeptide #4978.
XX
KW Recombinant DNA construct; transformed plant; improved plant property;
KW cold tolerance; heat tolerance; drought tolerance; herbicide; osmosis;
KW pathogen tolerance; pest tolerance; plant disease resistance;
KW cell cycle pathway modification; plant growth regulator;
KW homologous recombination; seed oil yield; protein yield; carbohydrate;
KW nitrogen; phosphorus; photosynthesis; lignin; galactomannan;
KW bacterial polypeptide.
XX
OS Bacteria.
XX
PN US2003233675-A1.
XX
PD 18-DEC-2003.
XX
PF 20-FEB-2003; 2003US-00369493.
XX
XX 21-FEB-2002; 2002US-0360039P.
XX
XX (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.

XX
PI Cao Y, Hinkle GJ, Slater SC, Chen X, Goldman BS;
XX WPI; 2004-061375/06.
XX
PT New recombinant DNA construct comprising a promoter positioned to provide
PT for expression of a polynucleotide encoding a polypeptide from a
PT microbial source, useful for producing plants with improved properties.
XX
PS Claim 1; SEQ ID NO 4978; 122pp; English.
XX
CC The invention relates to a recombinant DNA construct comprising a
CC promoter functional in a plant cell, where the promoter is positioned to
CC provide for expression of a polynucleotide encoding a polypeptide from a
CC microbial source. The invention also relates to a transformed plant
CC comprising the recombinant DNA construct and a method of producing a
CC transformed plant having an improved property. The plant is a crop plant
CC such as maize or soybean. The method of producing a transformed plant
CC having an improved property comprises transforming a plant with the
CC recombinant DNA construct and growing the transformed plant, where the
CC polynucleotide or polypeptide is useful for improving plant properties.
CC The recombinant DNA construct is useful for producing plants with
CC improved plant properties, e.g. improved cold, heat or drought tolerance,
CC tolerance to herbicides, extreme osmotic conditions, pathogens or pests,
CC increased resistance to plant disease, better growth rate by modification
CC of the cell cycle pathway with plant growth regulators, increased rate of
CC homologous recombination, modified seed oil or protein yield and/or
CC content, improved yield by modification of carbohydrate, nitrogen or
CC phosphorus use and/or uptake, by modification of photosynthesis or by
CC providing improved plant growth and development under at least one stress
CC condition, improved lignin production or improved galactomannan
CC production. This sequence represents a bacterial polypeptide used in the
CC scope of the invention. Note: The sequence data for this patent did not
CC form part of the printed specification but was obtained in electronic
CC format from USPTO at seqdata.uspto.gov/sequence.html.
XX
SQ Sequence 385 AA;
Query Match 51.6%; Score 79; DB 8; Length 385;
Best Local Similarity 51.6%; Pred. No. 0.018;
Matches 16; Conservative 7; Mismatches 8; Indels 0; Gaps 0;
QY 1 KEARKVSRGIDRLMDKRDLDQOQTHRLLLIG 31
Db 16 REARKVVKQIEQLAKDKQVMRATHRLLLIG 46
RESULT 10
AAB99072
ID AAB99072 standard; protein; 353 AA.
XX
AC AAB99072;
XX
DT 23-AUG-2001 (first entry)
XX
DE Human G-protein alpha subunit q.
XX
KW G-protein coupled receptor; GPCR; GnRH receptor; disease treatment;
KW gonadotrophin releasing; hormone receptor; hormone dependent cancer;
KW human; catfish; goldfish; cow; sheep; horse; fruitfly; pig; mouse;
KW gene therapy.
XX
OS Homo sapiens.
XX
PN WO200136446-A2.
XX
PD 25-MAY-2001.
XX
PF 17-NOV-2000; 2000WO-GB004385.
XX
XX 17-NOV-1999; 99GB-00027215.
XX
PA (UYBR-) UNIV BRISTOL.

```
XX Mcardle CA;
XX WPI; 2001-355607/37.
XX
XX Use of a vector encoding G-protein coupled receptors for manufacturing
XX medications for treating cancer, diseases of cardiovascular system,
XX nervous system, digestive system, immune system, or muscle diseases.
XX
XX Disclosure; Fig 19; 78pp; English.
XX
XX The present invention describes a prodrug comprising a vector encoding a
XX G-protein coupled receptor (GPCR). This can be used in the treatment of
XX diseases, including hormone-dependent cancers, cardiovascular, nervous
XX system, digestive system, immune system, respiratory, skeletal,
XX endocrine, sensory and muscle diseases and disorders. The present
XX sequence is a protein described in the exemplification of the invention
XX
XX Sequence 353 AA;
XX
XX Query Match 49.7%; Score 76; DB 4; Length 353;
XX Best Local Similarity 51.6%; Pred. NO. 0.043;
XX Matches 16; Conservative 7; Mismatches 8; Indels 0; Gaps 0;
XX
XX 1 KEARKVSRGIDRMRLRDQKRDLDQOQTHRLLLLG 31
XX |||||:|:|:| |||||:|:|:|
XX 10 KEARRINDEIERQLRRDKRDARRELKLLLG 40
XX
XX
XX RESULT 11
XX ABG68587
XX ID ABG68587 standard; protein; 353 AA.
XX
XX AC ABG68587;
XX
XX DT 07-OCT-2002 (first entry)
XX
XX DE Mouse G protein alpha sub-unit q family variant #3.
XX
XX KW G q protein; sensory signaling; chemoreceptor; tastant; olfactant;
XX pheromone; G protein alpha sub-unit; q family; G alpha q.
XX
XX OS Mus musculus.
XX
XX PN W0200236622-A2.
XX
XX PD 10-MAY-2002.
XX
XX PF 24-OCT-2001; 2001WO-US032619.
XX
XX PR 30-OCT-2000; 2000US-0243770P.
XX
XX PA (SENO-) SENOMYX INC.
XX
XX PI Yao Y, Xu H;
XX
XX DR WPI; 2002-519234/55.
XX
XX PT New G-alpha-q protein variants, useful for analyzing and discovering
XX agonists or antagonists of chemoreceptors, such as G protein coupled
XX receptors involved in sensing of tastants, olfactants or pheromones.
XX
XX PS Claim 13; Page 24; 32pp; English.
XX
XX CC The invention describes an isolated variant of a G q protein, which
XX exhibits increased promiscuity relative to the corresponding G q protein.
XX The variant is used to identify a compound that modulates sensory
XX signaling in sensory cells and to identify a compound that interacts with
XX the G q variant protein. The G q protein variant is useful for analysing
XX and discovering agonists or antagonists of chemoreceptors, such as G
XX protein coupled receptors involved in sensing of tastants, olfactants or
XX pheromones. This is the amino acid sequence of a G protein alpha sub-unit
XX q family (G alpha q) variant that can functionally couple to sensory cell
XX
XX Query Match 49.7%; Score 76; DB 5; Length 353;
XX Best Local Similarity 51.6%; Pred. NO. 0.043;
XX Matches 16; Conservative 7; Mismatches 8; Indels 0; Gaps 0;
XX
XX 1 KEARKVSRGIDRMRLRDQKRDLDQOQTHRLLLLG 31
XX |||||:|:|:| |||||:|:|:|
XX 10 KEARRINDEIERQLRRDKRDARRELKLLLG 40
XX
XX
XX RESULT 12
XX ABG68585
XX ID ABG68585 standard; protein; 353 AA.
XX
XX AC ABG68585;
XX
XX DT 07-OCT-2002 (first entry)
XX
XX DE Mouse G protein alpha sub-unit q family variant #1.
XX
XX KW G q protein; sensory signaling; chemoreceptor; tastant; olfactant;
XX pheromone; G protein alpha sub-unit; q family; G alpha q.
XX
XX OS Mus musculus.
XX
XX PN W0200236622-A2.
XX
XX PD 10-MAY-2002.
XX
XX PF 24-OCT-2001; 2001WO-US032619.
XX
XX PR 30-OCT-2000; 2000US-0243770P.
XX
XX PA (SENO-) SENOMYX INC.
XX
XX PI Yao Y, Xu H;
XX
XX DR WPI; 2002-519234/55.
XX
XX PT New G-alpha-q protein variants, useful for analyzing and discovering
XX agonists or antagonists of chemoreceptors, such as G protein coupled
XX receptors involved in sensing of tastants, olfactants or pheromones.
XX
XX PS Claim 13; Page 23; 32pp; English.
XX
XX CC The invention describes an isolated variant of a G q protein, which
XX exhibits increased promiscuity relative to the corresponding G q protein.
XX The variant is used to identify a compound that modulates sensory
XX signaling in sensory cells and to identify a compound that interacts with
XX the G q variant protein. The G q protein variant is useful for analysing
XX and discovering agonists or antagonists of chemoreceptors, such as G
XX protein coupled receptors involved in sensing of tastants, olfactants or
XX pheromones. This is the amino acid sequence of a G protein alpha sub-unit
XX q family (G alpha q) variant that can functionally couple to sensory cell
XX
XX Query Match 49.7%; Score 76; DB 5; Length 353;
XX Best Local Similarity 51.6%; Pred. NO. 0.043;
XX Matches 16; Conservative 7; Mismatches 8; Indels 0; Gaps 0;
XX
XX 1 KEARKVSRGIDRMRLRDQKRDLDQOQTHRLLLLG 31
XX |||||:|:~|:~| |||||:~|:~|:
XX 10 KEARRINDEIERQLRRDKRDARRELKLLLG 40
XX
XX
XX RESULT 13
XX
```



```

XX 28-JAN-2003; 2003WO-US002452.
PF XX
XX 28-JAN-2002; 2002US-0352720P.
PR XX
XX (BRIM ) BRISTOL-MYERS SQUIBB CO.
PA PA
PA (EXEL-) EXELIXIS INC.
XX XX
PI Moore L, Kindt RM, Kopczynski J, Doberstein SK, Cockett M;
PI Ramanathan C, Lodge N, Fitzgerald K, Stouch T;
XX DR
XX WPI; 2003-646090/61.
XX XX
XX Screening agents that modulate interaction of regulator of G-protein
PT signaling and Galphag, comprises contacting one of the proteins with a
PT candidate agent in an assay system and detecting the candidate agent-
PT biased activity of the system.
XX XX
XX Example 5; Fig 1B; 105pp; English.
XX XX
XX The invention relates to screening agents that modulate the interaction
CC of regulator of G-protein signaling (RGS) and Galphag proteins. The
CC method involves (a) contacting a screening assay system comprising a RGS
CC or Galphag polypeptide, with an agent; and (b) detecting an agent-biased
CC activity of the system, where a difference between the agent-biased and
CC reference activity indicates the modulatory action of the agent on RGS
CC and Galphag interaction. The method is useful for identifying agents that
CC modulate urinary incontinence. The modulators are useful for treating or
CC preventing urinary incontinence, depression, anxiety, arrhythmia,
CC cognitive disorders, psychosis, skeletal muscle disorders, cardiac muscle
CC disorders, smooth muscle disorders, muscle spasms, skeletal muscle
CC spasms, cardiac muscle spasms, smooth muscle spasms, muscle contraction
CC disorders, and muscle relaxation disorders. Sequences ABR82630-637
CC represent C. elegans Gq homologue, EGL-30 protein and related fragments
XX XX
SQ Sequence 353 AA;
Query Match 49.7%; Score 76; DB 7; Length 353;
Best Local Similarity 51.6%; Pred No: 0.043;
Matches 16; Conservative 7; Mismatches 8; Indels 0; Gaps 0;

Qy 1 KEARKVSRGIDRLRDQKRDQLQTHRLLLG 31
   |||::: |||::: |||::: |||:::
Db 10 KEARRINDEIERQLRRDKRDARRELKLLLG 40

Search completed: March 2, 2006, 19:32:18
Job time : 10.636 secs

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OM protein.: protein search, using sw model

Run on: March 2, 2006, 19:30:27 ; Search time 1.83845 Seconds
(without alignments)
1622.414 Million cell updates/sec

Title: US-10-618-320A-1_COPY_96_126
Perfect score: 153
Sequence: 1 KEARKVSRGIDRLMDQKEDLQOTHRLLLLG 31

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
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1: pir1.*
2: pir2.*
3: pir3.*
4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	79	51.6	375	2 T37245	GTP-binding regula
2	79	51.6	385	2 D87723	protein R06A10.2
3	76	49.7	359	2 S71963	GTP-binding protei
4	76	49.7	359	2 S45699	GTP-binding regula
5	72	47.1	846	2 S52418	GTP-binding regula
6	71	46.4	359	1 RGM5Q	GTP-binding protei
7	70	45.8	355	2 A40891	GTP-binding protei
8	68	44.4	353	2 B40891	GTP-binding protei
9	68	44.4	353	2 S34347	GTP-binding regula
10	68	44.4	354	2 S33309	GTP-binding regula
11	68	44.4	359	1 RGHUGY	GTP-binding regula
12	68	44.4	359	1 RGM511	GTP-binding regula
13	68	44.4	359	2 S30359	GTP-binding regula
14	68	44.4	360	2 JN0115	GTP-binding regula
15	67	43.8	381	2 I53271	G-protein alpha-o
16	65	42.5	355	2 A41534	GTP-binding protei
17	64	41.8	32	2 S36809	GTP-binding regula
18	64	41.8	91	2 A46685	GTP-binding regula
19	64	41.8	359	2 S45700	G-alpha-11 protein
20	64	41.8	377	1 RGM5A1	GTP-binding regula
21	64	41.8	379	2 A42964	guanine nucleotide
22	64	41.8	380	1 RGHUA1	GTP-binding regula
23	64	41.8	394	1 RGHVAE	GTP-binding regula
24	64	41.8	394	1 RGM5A2	GTP-binding regula
25	64	41.8	394	1 RGHYA2	GTP-binding regula
26	64	41.8	394	1 RGR7A2	GTP-binding regula
27	64	41.8	394	2 S33458	GTP-binding regula
28	64	41.8	395	1 RGHUA2	GTP-binding regula
29	64	41.8	397	1 RGPCA2	GTP-binding regula

30	63	41.2	379	1 RGXLA	GTP-binding regula
31	63	41.2	379	2 A41095	GTP-binding regula
32	63	41.2	381	2 A48071	guanine nucleotide
33	63	41.2	394	1 RGHOGA	GTP-binding regula
34	62	40.5	355	1 RGHUGX	GTP-binding regula
35	62	40.5	355	1 RGR7GX	GTP-binding regula
36	61	39.9	382	1 RGFPA5	GTP-binding regula
37	61	39.9	385	1 RGFPA1	GTP-binding regula
38	58	37.9	374	2 B41534	GTP-binding protei
39	58	37.9	645	2 S14992	dnak-type molecula
40	58	37.9	646	2 T46650	heat shock proteina
41	58	37.9	648	2 S53498	dnak-type molecula
42	58	37.9	785	2 AB1582	Muts protein (Muts
43	57	37.3	652	2 AS3163	dnak-type molecula
44	57	37.3	785	2 AH1228	Muts protein (Muts
45	56	36.6	355	2 T15288	hypothetical prote

ALIGNMENTS

RESULT 1

T37245

GTP-binding regulatory protein Gs alpha-S chain (adenylate cyclase-stimulating) - Caenorh
N;Alternate names: G protein a(s) subunit

C;Species: Caenorhabditis elegans

C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004

C;Accession: T37243; T37245

R;Park, J.; Ohshima, S.; Tani, T.; Ohshima, Y.

Gene 194, 183-190, 1997

A;Title: Structure and expression of the gsa-1 gene encoding a G protein alpha(s) subunit

A;Reference number: Z21641; MUID:97417487; PMID:9272860

A;Accession: T37243

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: mRNA

A;Residues: 1-375 <PAR>

A;Cross-references: UNIPROT:O18678; UNIPARC:UPI0000082C78; EMBL:AB003486; NID:92443297; 1

A;Experimental source: strain N2; mixed developmental stages

A;Accession: T37245

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: DNA

A;Residues: 1-375 <PA2>

A;Cross-references: UNIPARC:UPI0000082C78; EMBL:AB003487; PIDN:BAA22402.1

A;Experimental source: strain N2; mixed developmental stages

A;Gene: gsa-1

A;Map position: 1

A;Introns: 31/3; 85/3; 125/3; 158/2; 201/2; 246/2; 327/3

C;Superfamily: GTP-binding regulatory protein Gs alpha chain

C;Keywords: GTP binding; signal transduction

Query Match 51.6%; Score 79; DB 2; Length 375;
Best Local Similarity 51.6%; Pred. No. 0.0028; 8; Indels 0; Gaps 0;
Matches 16; Conservative 7; Mismatches 8;

OY 1 KEARKVSRGIDRLMDQKEDLQOTHRLLLLG 31

Db 13 REARKVVKQIEQLAKDKQVMRATHRLLLLG 43

RESULT 2

D87723

protein R06A10.2 [imported] - Caenorhabditis elegans

C;Species: Caenorhabditis elegans

C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004

C;Accession: D87723

R;anonymous, The C. elegans Sequencing Consortium.

A;Title: Genome sequence of the nematode C. elegans: a platform for investigating biology

A;Reference number: A75000; MUID:99069613; PMID:9851916

A;Note: see websites genome.wustl.edu/gsc/Celegans/ and www.sanger.ac.uk/projects/c_eleg

A;Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; and

A;Accession: D87723

A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-385 <STO>
A;Cross-references: UNIPROT:O18678; UNIPARC:UPI0000177887; GB:chr_I; PIDN:AAB96733.1; PID:
C;Genetics:
A;Gene: R06A10.2
A;Map position: 1
C;Superfamily: GTP-binding regulatory protein Gs alpha chain

Query Match 51.6%; Score 79; DB 2; Length 385;
Best Local Similarity 51.6%; Pred. No. 0.0029; 8; Indels 0; Gaps 0;
Matches 16; Conservative

QY 1 KEARKVSRGIDRMRLDQKRDQLQOQTHRLLLG 31
DB 16 REARKVVKQIEEQQLAKDQKQWRATHRLLLG 46

RESULT 3
S71963
GTP-binding protein alpha-q - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 29-Jan-1998 #sequence_revision 06-Feb-1998 #text_change 02-Feb-2001
C;Accession: S71963
R;Johnson, G.J.; Leis, L.A.; Dunlop, P.C.
Biochem. J. 318, 1023-1031, 1996
A;Title: Specificity of G-alpha(q) and G-alpha(11) gene expression in platelets and erythrocytes
A;Reference number: S71963; MUID:96433124; PMID:8836152
A;Accession: S71963
A;Molecule type: mRNA
A;Residues: 1-359 <JOH>
A;Cross-references: UNIPARC:UPI000016AC08; EMBL:L76256; NID:g1478071; PIDN:AAB39498.1; PID:
C;Superfamily: GTP-binding regulatory protein Gs alpha chain
C;Keywords: GTP binding; nucleotide binding; P-loop; signal transduction
F;46-53/Region: nucleotide-binding motif A (P-loop)
F;274-277/Region: GTP-binding NKXD motif

Query Match 49.7%; Score 76; DB 2; Length 359;
Best Local Similarity 51.6%; Pred. No. 0.0069; 8; Indels 0; Gaps 0;
Matches 16; Conservative 7; Mismatches 8; Indels 0; Gaps 0;

QY 1 KEARKVSRGIDRMRLDQKRDQLQOQTHRLLLG 31
DB 16 KEARRINDEIERQLRRDKRDARRELKLLLG 46

RESULT 4
S45699
GTP-binding regulatory protein alpha chain q - African clawed frog
N;Alternate names: G-alpha-q protein
C;Species: Xenopus laevis (African clawed frog)
C;Date: 10-Dec-1994 #sequence_revision 10-Nov-1995 #text_change 02-Feb-2001
C;Accession: S45699
R;Shapira, H.; Way, J.; Lipinsky, D.; Oron, Y.; Battey, J.F.
FEBS Lett. 348, 89-92, 1994
A;Title: Neuromedin B receptor, expressed in Xenopus laevis oocytes, selectively couples with G-protein
A;Reference number: S45699; MUID:94289861; PMID:8026589
A;Accession: S45699
A;Molecule type: mRNA
A;Residues: 1-359 <SHA>
A;Cross-references: UNIPARC:UPI0000171485; GB:U10502; NID:g505689; PIDN:AAAS2189.1; PID:
C;Superfamily: GTP-binding regulatory protein Gs alpha chain
C;Keywords: GTP binding; nucleotide binding; P-loop; signal transduction
F;46-53/Region: nucleotide-binding motif A (P-loop)
F;274-277/Region: GTP-binding NKXD motif
F;52/Binding site: GTP (Lys) #status predicted
F;183/Modified site: ADP-ribosylarginine (Arg) (by cholera toxin) #status predicted

Query Match 49.7%; Score 76; DB 2; Length 359;
Best Local Similarity 51.6%; Pred. No. 0.0069; 8; Indels 0; Gaps 0;
Matches 16; Conservative 7; Mismatches 8; Indels 0; Gaps 0;

QY 1 KEARKVSRGIDRMRLDQKRDQLQOQTHRLLLG 31

DB 16 KEARRINDEIERQLRRDKRDARRELKLLLG 46

RESULT 5
S52418
GTP-binding regulatory protein Gs alpha-XL chain - rat
N;Alternate names: G protein XL-alpha-s
C;Species: Rattus norvegicus (Norway rat)
C;Date: 14-Jul-1995 #sequence_revision 10-Nov-1995 #text_change 02-Feb-2001
C;Accession: S52418
R;Kehlenbach, R.H.; Matthey, J.; Huttner, W.B.
Nature 372, 804-809, 1994
A;Title: XL-alpha-s is a new type of G protein.
A;Reference number: S52418; MUID:95089824; PMID:7997272
A;Accession: S52418
A;Molecule type: mRNA
A;Residues: 1-846 <KEH>
A;Cross-references: UNIPARC:UPI000017C91F; EMBL:X84047; NID:g642267; PIDN:CAAS8866.1; PID:
R;Kehlenbach, R.H.; Matthey, J.; Huttner, W.B.
Nature 375, 253, 1995
A;Title: Correction: Xlalphas is a new type of G protein.
A;Reference number: S58911
A;Contents: annotation; assignment of start_codon
A;Note: experimental data from this paper suggest that the translation is initiated at pC
C;Keywords: GTP binding; nucleotide binding; P-loop; signal transduction
F;132-846/Product: GTP-binding regulatory protein Gs alpha-XL chain #status experimental
F;499-506/Region: nucleotide-binding motif A (P-loop)
F;744-747/Region: GTP-binding NKXD motif

Query Match 47.1%; Score 72; DB 2; Length 846;
Best Local Similarity 53.6%; Pred. No. 0.063; 8; Indels 0; Gaps 0;
Matches 15; Conservative 5; Mismatches 8; Indels 0; Gaps 0;

QY 4 RKVSRGIDRMRLDQKRDQLQOQTHRLLLG 31
DB 472 KRRSLIDKQLEERKDYMCYTHRLLLG 499

RESULT 6
RGMSQ
GTP-binding regulatory protein Gq alpha chain - mouse
N;Alternate names: guanine nucleotide binding protein Gq alpha chain; heterotrimeric G-p
C;Species: Mus musculus (house mouse)
C;Date: 31-Dec-1992 #sequence_revision 31-Dec-1992 #text_change 09-Jul-2004
C;Accession: A38414
R;Strathmann, M.; Simon, M.I.
Proc. Natl. Acad. Sci. U.S.A. 87, 9113-9117, 1990
A;Title: G protein diversity: a distinct class of alpha subunits is present in vertebrate
A;Reference number: A38414; MUID:91067657; PMID:2123549
A;Accession: A38414
A;Molecule type: mRNA
A;Residues: 1-359 <STR>
A;Cross-references: UNIPROT:P21279; UNIPARC:UPI0000161D60; GB:M55412; NID:g193501; PIDN:
C;Comment: The G proteins are a family of guanine nucleotide-binding proteins that relay
cins. The beta and gamma chains, required for GTPase activity, appear to be common to all
rase; it is specific for each type of G protein.
C;Superfamily: GTP-binding regulatory protein Gs alpha chain
C;Keywords: GTP binding; heterotrimer; nucleotide binding; P-loop; signal transduction
F;46-53/Region: nucleotide-binding motif A (P-loop)
F;274-277/Region: GTP-binding NKXD motif
F;52/Binding site: GTP (Lys) #status predicted
F;183/Modified site: ADP-ribosylarginine (Arg) (by cholera toxin) #status predicted

Query Match 46.4%; Score 71; DB 1; Length 359;
Best Local Similarity 48.4%; Pred. No. 0.034; 8; Indels 0; Gaps 0;
Matches 15; Conservative 8; Mismatches 8; Indels 0; Gaps 0;

QY 1 KEARKVSRGIDRMRLDQKRDQLQOQTHRLLLG 31
DB 16 KEARRINDEIERHVRDRDKRDARRELKLLLG 46

A;Cross-references: UNIPROT:P38411; UNIPARC:UPI000012B263; EMBL:Z23106; NID:g312629; PID:
C;Superfamily: GTP-binding regulatory protein Gs alpha chain
C;Keywords: GTP binding; heterotrimer; nucleotide binding; P-loop; signal transduction
F;40-48/Region: nucleotide-binding motif A (P-loop)
F;150-152/Region: GTP-binding SAK/L motif
F;268-271/Region: GTP-binding NKXD motif
F;46/Binding site: GTP (lys) #status predicted
F;177/Modified site: ADP-ribosylarginine (Arg) (by cholera toxin) #status predicted

Query Match 44.4%; Score 68; DB 2; Length 353;
Best Local Similarity 41.9%; Pred. No. 0.087;
Matches 13; Conservative 10; Mismatches 8; Indels 0; Gaps 0;

Oy 1 KEARKVSGIDRMRLDQKRDQQTHRLLLLG 31
|| :|::| |::| |::| |::| |::|
Db 10 KEQKRINQEIERQLKRDKDARRELKLLLG 40

RESULT 10
S33309
GTP-binding regulatory protein Gq alpha chain - northern European squid
C;Species: Loligo forbesi (northern European squid)
C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 09-Jul-2004
C;Accession: S33309
R;Ryba, N.J.P.; Findlay, J.B.C.; Reid, J.D.
Biochem. J. 292, 333-341, 1993
A;Title: The molecular cloning of the squid (Loligo forbesi) visual Gq-alpha subunit and
A;Reference number: S33309; MUID:93277493; PMID:9503868
A;Accession: S33309
A>Status: preliminary
A:Molecule type: mRNA
A;Residues: 1-354 (RYB>
A;Cross-references: UNIPROT:P38412; UNIPARC:UPI000012B262; EMBL:L10289
C;Superfamily: GTP-binding regulatory protein Gs alpha chain
C;Keywords: GTP binding; nucleotide binding; P-loop
F;40-47/Region: nucleotide-binding motif A (P-loop)
F;150-152/Region: GTP-binding SAK/L motif
F;269-272/Region: GTP-binding NKXD motif

Query Match 44.4%; Score 68; DB 2; Length 354;
Best Local Similarity 41.9%; Pred. No. 0.088;
Matches 13; Conservative 10; Mismatches 8; Indels 0; Gaps 0;

Oy 1 KEARKVSGIDRMRLDQKRDQQTHRLLLLG 31
|| :|::| |::| |::| |::| |::|
Db 10 KEQKRINQEIERQLKRDKDARRELKLLLG 40

RESULT 11
RGHUGY
GTP-binding regulatory protein Gy alpha chain - human
N;Alternate names: guanine nucleotide binding protein Gy alpha chain; heterotrimeric G-protein
C;Species: Homo sapiens (man)
C;Date: 31-Dec-1992 #sequence_revision 31-Dec-1992 #text_change 09-Jul-2004
C;Accession: A39394
R;Jiang, M.; Pandey, S.; Tran, V.T.; Fong, H.K.W.
Proc. Natl. Acad. Sci. U.S.A. 89, 3907-3911, 1991
A;Title: Guanine nucleotide-binding regulatory proteins in retinal pigment epithelial cells
A;Reference number: A39394; MUID:91219481; PMID:1902575
A;Accession: A39394
A:Molecule type: mRNA
A;Residues: 1-359 (JTA>
A;Cross-references: UNIPROT:P29992; UNIPARC:UPI0000161B28; GB:M69013; NID:g183690; PIDN:/
C;Comment: The G proteins are a family of guanine nucleotide-binding proteins that relay
signals. The beta and gamma chains, required for GTPase activity, appear to be common to all
types. It is specific for each type of G protein.

A;Gene: GDB:GN11
A;Cross-references: GDB:132587; OMIM:139313
A;Map position: 19p13.3-19p13.3
C;Superfamily: GTP-binding regulatory protein Gs alpha chain
C;Keywords: GTP binding; heterotrimer; nucleotide binding; P-loop; signal transduction
F;46-53/Region: nucleotide-binding motif A (P-loop)

Search completed: March 2, 2006, 19:31:05
Job time : 1.83845 secs

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GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: March 2, 2006, 19:29:50 ; Search time 19.3988 Seconds
(without alignments)
1127.462 Million cell updates/sec

Title: US-10-618-320a-1_copy_96_126

Perfect score: 153

Sequence: 1 KEARKVSRGIDRLMDKRDQLQTHRLLLG 31

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

UniProt 05.80.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	153	100.0	458	2	Q86XU3 HUMAN
2	149	97.4	230	2	Q8BH88 MOUSE
3	149	97.4	448	2	Q66L47 MOUSE
4	115	75.2	462	2	Q6GLL1 XENLA
5	95	62.1	351	2	Q8N2B4 HUMAN
6	79	51.6	374	2	Q60PW5 CAEBR
7	79	51.6	375	2	Q4VT24 CAEBR
8	79	51.6	375	2	Q18678 CAEBL
9	78	51.0	485	2	Q4SQ90 TETNG
10	76	49.7	353	1	GNAQ CANFA
11	76	49.7	353	1	GNAQ HUMAN
12	76	49.7	353	1	GNAQ MOUSE
13	76	49.7	353	1	GNAQ RAT
14	76	49.7	359	2	Q6NT27 HUMAN
15	76	49.7	359	2	Q5F3B5 CHICK
16	76	49.7	359	2	Q66I28 XENLA
17	76	49.7	502	2	Q4RT50 TETNG
18	73	47.7	377	2	Q4RT50 TETNG
19	72	47.1	177	2	Q6TP31 PINFU
20	72	47.1	353	1	GNAQ HUMAN
21	72	47.1	353	1	GNAQ XENLA
22	72	47.1	353	2	P91955 LIMPO
23	72	47.1	353	2	Q58FC0 HELAM
24	72	47.1	353	2	Q8T6P8 NAMBR
25	72	47.1	353	2	Q9U473 PANAR
26	72	47.1	353	2	Q6ITD0 PENVA
27	72	47.1	359	2	Q76FN3 BOMWO
28	72	47.1	359	2	Q5RKP9 BRARE
29	72	47.1	715	2	Q63803 RAT
30	72	47.1	756	2	Q9ZLN8 MOUSE
31	72	47.1	827	2	Q6R0H4 MOUSE

32	72	47.1	876	2	Q6R0H5 MOUSE
33	72	47.1	1133	2	Q6R0H7 MOUSE
34	71	46.4	353	2	Q9NF20 CALVI
35	71	46.4	353	2	Q9NL92 OCTVU
36	71	46.4	353	2	Q7PHK0 ANOGLA
37	71	46.4	353	2	Q7PHK1 ANOGLA
38	71	46.4	353	2	Q6W9M4 PENVA
39	71	46.4	367	2	Q4RMQ6 TETNG
40	70	45.8	92	2	Q5JW64 HUMAN
41	70	45.8	185	2	Q5JW68 HUMAN
42	70	45.8	188	2	Q5JW68 HUMAN
43	70	45.8	193	2	Q5JW69 HUMAN
44	70	45.8	355	1	GNA14 BOVIN
45	70	45.8	355	1	GNA14 HUMAN

Q6R0H5	mus musculu
Q6R0H7	mus musculu
Q9NF20	calliphora
Q9NL92	octopus vul
Q7PHK0	anopheles g
Q7PHK1	anopheles g
Q6W9M4	penicillium
Q4RMQ6	tetradodon n
Q5JW64	homo sapien
Q5JW68	homo sapien
Q5JW68	homo sapien
Q5JW69	homo sapien
P38408	bos taurus
Q95837	homo sapien

ALIGNMENTS

RESULT 1
Q86XU3 HUMAN PRELIMINARY; PRT; 458 AA.
AC Q86XU3;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Guanine nucleotide binding protein (G protein), alpha activating
DE activity polypeptide, olfactory type, isoform 1.
GN Names=GNAL;
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Testis;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heien F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaby S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettaman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield J.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnurch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Testis;
RA NIH MGC Project;
RG Submitted (APR-2003) to the EMBL/GenBank/DBJ databases.
RL EMBL; BC050021; AAH50021.1; -, mRNA.
DR HSSP; P04896; 1CJU.
DR SMR; Q86XU3; 117-455.
DR Ensembl; ENSG00000141404; Homo sapiens.
DR GO; GO:0005525; F:GTP binding; IEA.
DR GO; GO:0004871; F:signal transducer activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. . . ; IEA.
DR GO; GO:0007165; P:signal transduction; IEA.
DR InterPro; IPR01019; Gprotein_alpha_bd.
DR InterPro; IPR000367; Gprotein_alpha_s.

DR GO; GO:0007190; P:adenylylate cyclase activation; IDA.
 DR GO; GO:0007608; P:perception of smell; IMP.
 DR InterPro; IPR011025; GproteinA_insert.
 DR InterPro; IPR001019; Gprotein_alpha.
 DR InterPro; IPR000367; Gprotein_alpha_s.
 DR Pfam; PF00503; G-alpha; 1.
 DR PRINTS; PR00443; GPROTEINAS.
 DR ProDom; PD000281; Gprotein_alpha; 1.
 DR SMART; SM00275; G_alpha; 1.
 SQ SEQUENCE 230 AA; 25632 MW; 0BE3051094E326C2 CRC64;

Query Match 97.4%; Score 149; DB 2; Length 230;
 Best Local Similarity 96.8%; Pred. No. 2 Re-12;
 Matches 30; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KEARKVSRGIDRLMLRDLQKRDLOQTHRLLLG 31
 |||||
 DB 86 KEARKVSRGIDRLMLRDLQKRDLOQTHRLLLG 116

RESULT 3

Q66L47 MOUSE
 ID Q66L47 MOUSE PRELIMINARY; PRT; 448 AA.
 AC Q66L47;
 DT 25-OCT-2004 (TrEMBLrel. 28, Created)
 DT 23-OCT-2004 (TrEMBLrel. 28, Last sequence update)
 DT 23-OCT-2004 (TrEMBLrel. 28, Last annotation update)
 DE Gnal protein.
 GN Names=Gnal;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muridae; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP NUCLEOTIDE SEQUENCE
 RC STRAIN=C57BL/6; TISSUE=Brain;
 RX MEDLINE=223388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Udell T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Villalón D.K., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickinson M.C.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallos D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6; TISSUE=Brain;
 RG NIH MGC Project;
 RL Submitted (JUL-2004) to the EMBL/GenBank/DBJ databases.
 DR ENBL; BC078439; AAH78439.1; -; mRNA.
 DR SNR; Q66L47; 107-445.
 DR Ensembl; ENSMUSG0000024524; Mus musculus.
 DR MGI; MGI:95774; Gnal.
 DR GO; GO:0007190; P:adenylylate cyclase activation; IDA.
 DR GO; GO:0007608; P:perception of smell; IMP.
 DR InterPro; IPR001019; Gprotein_alpha.
 DR InterPro; IPR000367; Gprotein_alpha_s.
 DR InterPro; IPR011025; GproteinA_insert.
 DR Pfam; PF00503; G-alpha; 1.

DR PRINTS; PR00318; GPROTEINA.
 DR PRINTS; PR00443; GPROTEINAS.
 DR ProDom; PD000281; Gprotein_alpha; 1.
 DR SMART; SM00275; G_alpha; 1.
 SQ SEQUENCE 448 AA; 51357 MW; AE192038B7E3B40E CRC64;

Query Match 97.4%; Score 149; DB 2; Length 448;
 Best Local Similarity 96.8%; Pred. No. 5.6e-12;
 Matches 30; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KEARKVSRGIDRLMLRDLQKRDLOQTHRLLLG 31
 |||||
 DB 86 KEARKVSRGIDRLMLRDLQKRDLOQTHRLLLG 116

RESULT 4

Q6GLL1 XENLA
 ID Q6GLL1_XENLA PRELIMINARY; PRT; 462 AA.
 AC Q6GLL1;
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE LOC443714 protein (Fragment).
 GN Names=LOC443714;
 OS Xenopus laevis (African clawed frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
 OC Xenopodinae; Xenopus; Xenopus.
 OX NCBI_TaxID=8355;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Brain;
 RX MEDLINE=223388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Udell T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickinson M.C.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallos D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Brain;
 RX MEDLINE=223411132; PubMed=12454917; DOI=10.1002/gvdy.10174;
 RA Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
 RA Richardson P.;
 RT "Genetic and genomic tools for Xenopus research: The NIH Xenopus
 Dev. Dyn. 225:384-391(2002).
 RN [3]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Brain;
 RA Klein S., Gerhard D.S.;
 RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
 DR ENBL; BC074466; AAH74466.1; -; mRNA.
 DR SNR; Q6GLL1; 120-459.
 DR GO; GO:0005525; F:GTP binding; IEA.
 DR GO; GO:0004871; F:signal transducer activity; IEA.
 DR GO; GO:0007186; P:G-protein coupled receptor protein signalin.; IEA.
 DR GO; GO:0007165; P:signal transduction; IEA.

DR InterPro: IPR011025; G-protein insert.
 DR InterPro: IPR001019; G-protein_alpha.
 DR InterPro: IPR000367; G-protein_alpha_s.
 DR InterPro: IPR002885; PPR.
 DR Pfam: PF00503; G-alpha; 1.
 DR PRINTS: PR00318; GPROTEINA.
 DR PRINTS: PR00443; GPROTEINA.
 DR ProDom: PD000281; G-protein_alpha; 1.
 DR SMART: SM00275; G-alpha; 1.
 FT TIGRFAMs: TIGR00756; PPR; 1.
 FT NON TER 1
 SQ SEQUENCE 462 AA; 53392 MW; 57EB03C65C17DAF4 CRC64;

Query Match 75.2%; Score 115; DB 2; Length 462;
 Best Local Similarity 71.0%; Pred. No. 2.9e-07;
 Matches 25; Conservative 7; Mismatches 2; Indels 0; Gaps 0;

QY 1 KEARKVSRGIDRLMDQKRDQLQOQTHRLLLLG 31
 |||:||||:||||:||||:||||:|||||
 Db 100 KEARKVSKTIDRLVLEQKREYKQTHRLLLLG 130

RESULT 5
 Q8N2B4_HUMAN
 ID Q8N2B4_HUMAN PRELIMINARY; PRT; 351 AA.
 AC Q8N2B4_2002 (TrEMBLrel. 22, Created)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE Hypothetical protein FLJ33549.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
 OC Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Amalgam; DOI=10.1038/ng1285;
 RX PubMed=14702039; Otsuki T., Sugiyama T., Irie R.,
 RA Ota T., Suzuki Y., Nishikawa T., Otsuki T., Sugiyama T., Irie R.,
 RA Wakamatsu A., Hayashi K., Sato K., Kimura K., Makita H.,
 RA Sekine M., Obayashi M., Nishi T., Shibahara T., Tanaka T., Ishii S.,
 RA Yamamoto J.-I., Saito K., Kawai Y., Isono Y., Nakamura Y.,
 RA Nagahori K., Murakami K., Yasuda T., Iwayanagi T., Wagatsuma M.,
 RA Shiratori A., Sudo H., Hosoiri T., Kaku Y., Kodaira H., Kondo H.,
 RA Sugawara M., Takahashi M., Kanda K., Yokoi T., Furuya T., Kikkawa E.,
 RA Omura Y., Abe K., Kamiyama K., Katsuta N., Sato K., Tanikawa M.,
 RA Yamazaki M., Ninomiya K., Ishibashi T., Yamashita H., Murakawa K.,
 RA Fujimori K., Tanai H., Kimata M., Watanabe M., Hiraoa S., Chiba Y.,
 RA Ishida S., Ono Y., Takiguchi S., Watanabe S., Yosida M., Hotuta T.,
 RA Kuano J., Kanehori K., Takahashi-Fujii A., Hara H., Tanase T.-O.,
 RA Nomura Y., Togiya S., Komai F., Hara R., Takeuchi K., Arita M.,
 RA Inose N., Musashino K., Yuuki H., Oshima A., Sasaki N., Aotsuka S.,
 RA Yoshikawa Y., Matsunawa H., Ichihara T., Shiohata N., Sano S.,
 RA Moriya S., Momiyama H., Satoh N., Takami S., Terashima Y., Suzuki O.,
 RA Nakagawa S., Senoh A., Mizoguchi H., Goto Y., Shimizu F., Wakemi B.,
 RA Hishigaki H., Watanabe T., Sugiyama A., Takemoto M., Kawakami B.,
 RA Yamazaki M., Watanabe K., Kumagai A., Itakura S., Fukuzumi Y.,
 RA Fujimori Y., Komiyama M., Tashiro H., Tanigami Y., Fujiwara T.,
 RA Ono T., Yamada K., Fujii Y., Ozaki K., Hirao M., Ohmori Y.,
 RA Okitani R., Kawakami T., Noguchi S., Itoh T., Shigeta K., Senba T.,
 RA Matsumura K., Nakajima Y., Mizuno T., Morinaga M., Komatsu T.,
 RA Togashi T., Oyama H., Hata H., Watanabe M., Komatsu T.,
 RA Mizushima-Sugano J., Satoh T., Shirai Y., Takahashi Y., Nakagawa K.,
 RA Okumura K., Nagase T., Nomura N., Kikuchi H., Masuho Y., Yamashita R.,
 RA Nakai K., Yada T., Nakamura Y., Ohara O., Isogai T., Sugano S.;
 RT "Complete sequencing and characterization of 21,243 full-length human
 cDNAs.";
 RL Nat. Genet. 36:40-45 (2004).
 DR EMBL; AK090868; BAC03535.1; -; mRNA.
 DR HSP; P04896; 1CJU.
 DR SMR; Q8N2B4; 10-348.

DR GO: 0005525; F-GTP binding; IEA.
 DR GO: 0004871; F-signal transducer activity; IEA.
 DR GO: 0007186; P-G-protein coupled receptor protein signalin. .; IEA.
 DR GO: 0007165; P-signal transduction; IEA.
 DR InterPro: IPR011025; G-protein_alpha_insert.
 DR InterPro: IPR001019; G-protein_alpha.
 DR InterPro: IPR000367; G-protein_alpha_s.
 DR Pfam: PF00503; G-alpha; 1.
 DR PRINTS: PR00318; GPROTEINA.
 DR PRINTS: PR00443; GPROTEINA.
 DR ProDom: PD000281; G-protein_alpha; 1.
 DR SMART: SM00275; G-alpha; 1.
 SQ SEQUENCE 351 AA; 41057 MW; 4956B9D7573F9F60 CRC64;

Query Match 62.1%; Score 95; DB 2; Length 351;
 Best Local Similarity 100.0%; Pred. No. 0.00013;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 MLRDQKRDQLQOQTHRLLLLG 31
 |||:||||:||||:||||:||||:|||||
 Db 1 MLRDQKRDQLQOQTHRLLLLG 19

RESULT 6
 Q60PW5_CABR
 ID Q60PW5_CABR PRELIMINARY; PRT; 374 AA.
 AC Q60PW5_2004 (TrEMBLrel. 28, Created)
 DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
 DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
 DE Hypothetical protein CBG22078.
 GN Names=CBG22078;
 OS Caenorhabditis briggsae.
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
 OC Rhabditidae; Peloderinae; Caenorhabditis.
 OX NCBI_TaxID=6238;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RG The C.briggsae Sequencing Consortium;
 RL Submitted (SEP-2003) to the EMBL/GenBank/DBJ databases.
 CC -!- CAUTION: The sequence shown here is derived from an
 CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
 CC preliminary data.
 DR EMBL; CAAC01000129; CAE74357.1; -; Genomic DNA.
 DR SMR; Q60PW5; 31-371.
 DR GO: 0005525; F-GTP binding; IEA.
 DR GO: 0004871; F-signal transducer activity; IEA.
 DR GO: 0007186; P-G-protein coupled receptor protein signalin. .; IEA.
 DR GO: 0007165; P-signal transduction; IEA.
 DR InterPro: IPR011025; G-protein_alpha_insert.
 DR InterPro: IPR001019; G-protein_alpha.
 DR InterPro: IPR000367; G-protein_alpha_s.
 DR Pfam: PF00503; G-alpha; 1.
 DR PRINTS: PR00318; GPROTEINA.
 DR PRINTS: PR00443; GPROTEINA.
 DR ProDom: PD000281; G-protein_alpha; 1.
 DR SMART: SM00275; G-alpha; 1.
 KW Hypothetical protein.
 SQ SEQUENCE 374 AA; 43851 MW; 2508543ED25CDF79 CRC64;

Query Match 51.6%; Score 79; DB 2; Length 374;
 Best Local Similarity 51.6%; Pred. No. 0.022;
 Matches 16; Conservative 7; Mismatches 8; Indels 0; Gaps 0;

QY 1 KEARKVSRGIDRLMDQKRDQLQOQTHRLLLLG 31
 |||:||||:||||:||||:||||:|||||
 Db 13 REARKVKNQIEQLAKDKQVMRATHRLLLLG 43

RESULT 7
 Q4VT24_CABR
 ID Q4VT24_CABR PRELIMINARY; PRT; 375 AA.
 AC Q4VT24;

DT 13-SEP-2005 (TReMBLrel. 31, Created)
 DT 13-SEP-2005 (TReMBLrel. 31, Last sequence update)
 DT 13-SEP-2005 (TReMBLrel. 31, Last annotation update)
 DE Gsa-1.
 OS Caenorhabditis briggsae.
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
 OC Rhabditidae; Peloderinae; Caenorhabditis.
 OX NCBI_TaxID=6238;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=AF16;
 RA Jovelin R., Phillips P.C.;
 RT "Functional constraint and divergence in the G protein family in
 RT Caenorhabditis elegans and Caenorhabditis briggsae."
 RL Submitted (MAY-2004) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AY634306; AAW02912.1; -; Genomic DNA.
 SQ SEQUENCE 375 AA; 43979 MW; D843530DAD61D42A CRC64;

 Query Match 51.6%; Score 79; DB 2; Length 375;
 Best Local Similarity 51.6%; Pred. No. 0.022;
 Matches 16; Conservative 7; Mismatches 8; Indels 0; Gaps 0;

 Qy 1 KEARKVSRGIDRMLRDKRDLQOQTHRLLLLG 31
 Db 13 REARKVKNQIEQLAKDKQVWRATHRLLLLG 43

 RESULT 8
 O18678 CAEBL
 ID O18678 CAEBL PRELIMINARY; PRT; 375 AA.
 AC O18678; 044744;
 DT 01-JAN-1998 (TReMBLrel. 05, Created)
 DT 01-JAN-1998 (TReMBLrel. 05, Last sequence update)
 DT 13-SEP-2005 (TReMBLrel. 31, Last annotation update)
 DE Heterotrimeric G protein alpha subunit (G protein, subunit alpha
 DE protein 1) (G protein a(S) subunit).
 GN Name=gsa-1; ORFNames=R06A10.2;
 OS Caenorhabditis elegans.
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
 OC Rhabditidae; Peloderinae; Caenorhabditis.
 OX NCBI_TaxID=6239;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=N2;
 RX MEDLINE=37417487; PubMed=9272860; DOI=10.1016/S0378-1119(97)00122-4;
 RA Park J., Ohshima S., Tani T., Ohshima Y.;
 RT "Structure and expression of the gsa-1 gene encoding a G protein
 RT alpha(s) subunit in C. elegans."
 RL Gene 194:183-190(1997).
 RN [2]
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
 RC STRAIN=Bristol N2;
 RX MEDLINE=99069613; PubMed=9851916;
 RG The C. elegans sequencing consortium;
 RT "Genome sequence of the nematode C. elegans: a platform for
 RT investigating biology."
 RL Science 282:2012-2018(1998).
 RN [3]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=N2;
 RA Cuppen E., Jansen G., Plasterk R.H.A.;
 RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AB003487; BAA22402.1; -; Genomic DNA.
 DR EMBL; AF019715; AAB96733.2; -; Genomic DNA.
 DR EMBL; AY008141; AAC32094.1; -; mRNA.
 DR EMBL; AB003486; BAA22401.1; -; mRNA.
 DR PIR; D87723; D87723.
 DR PIR; T37243; T37245.
 DR HSSP; P04896; 1CJU.
 DR SRR; O18678; 31-372.
 DR Ensembl; R06A10.2; Caenorhabditis elegans.
 DR WormBase; WBGene00001745; gsa-1.
 DR WormPep; R06A10.2; CE21115.

DR GO; GO:0005525; F:GTP binding; IEA.
 DR GO; GO:0004871; F:signal transducer activity; IEA.
 DR GO; GO:0007186; P:G-protein coupled receptor protein signalin.; IEA.
 DR GO; GO:0007165; P:signal transduction; IEA.
 DR InterPro; IPR001019; Gprotein_alpha.
 DR InterPro; IPR000367; Gprotein_alpha.S.
 DR InterPro; IPR011025; GproteinA_insert.
 DR Pfam; PF00503; G-alpha; 1.
 DR PRINTS; PR00318; GPROTEIN.
 DR PRINTS; PR00443; GPROTEINAS.
 DR SMART; SM00275; G_alpha; 1.
 KW Complete proteome.
 SQ SEQUENCE 375 AA; 44012 MW; B02C195E9191DD52 CRC64;

 Query Match 51.6%; Score 79; DB 2; Length 375;
 Best Local Similarity 51.6%; Pred. No. 0.022;
 Matches 16; Conservative 7; Mismatches 8; Indels 0; Gaps 0;

 Qy 1 KEARKVSRGIDRMLRDKRDLQOQTHRLLLLG 31
 Db 13 REARKVKNQIEQLAKDKQVWRATHRLLLLG 43

 RESULT 9
 Q4SQ90 TETNG
 ID Q4SQ90 TETNG PRELIMINARY; PRT; 485 AA.
 AC Q4SQ90;
 DT 13-SEP-2005 (TReMBLrel. 31, Created)
 DT 13-SEP-2005 (TReMBLrel. 31, Last sequence update)
 DT 13-SEP-2005 (TReMBLrel. 31, Last annotation update)
 DE Chromosome 4 SCAFI4533, whole genome shotgun sequence.
 DE (Fragment).
 GN ORFNames=GSTENG00014468001;
 OS Tetraodon nigroviridis (Green puffer).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
 OC Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
 OC Tetraodontidae; Tetraodontidae; Tetraodon.
 OX NCBI_TaxID=99883;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RA Jaillon O., Aury J.M., Brunet F., Petit J.L., Stange-Thomann N.,
 RA Mauceli E., Bouneau L., Fischer C., Ozouf-Costaz C., Bernot A.,
 RA Nicaud S., Jaffe D., Fisher S., Lutfalla G., Dossat C., Segurens B.,
 RA Dasilva C., Salanoubat M., Levy M., Boudet N., Castellano S.,
 RA Anthouard V., Jubin C., Castelli V., Katinka M., Vacherie B.,
 RA Biemont C., Skalli Z., Cattolico L., Poulin J., De Berardinis V.,
 RA Cruaud C., Duprat S., Brottier P., Coutanceau J.P., Guzy J.,
 RA Parra G., Lardier G., Chapple C., McKernan K.J., McEwan P., Bosak S.,
 RA Kellis M., Volff J.N., Guigo R., Zody M.C., Mesirov J.,
 RA Lindblad-Toh K., Birren B., Nuebaum C., Kahn D., Robinson-Rechavi M.,
 RA Laudet V., Schachter V., Quetier F., Saurin W., Scarpelli C.,
 RA Wincker P., Lander E.S., Weissbach J., Roest Crolius H.;
 RT "Genome duplication in the teleost fish Tetraodon nigroviridis reveals
 RT the early vertebrate proto-karyotype."
 RL Nature 431:946-957(2004).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RG Genoscope; Whitehead Institute Centre for Genome Research;
 RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.
 CC -!- CAUTION: The sequence shown here is derived from an
 CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
 CC preliminary data.
 DR EMBL; CAAE01014533; CAF97192.1; -; Genomic DNA.
 FT NON_TER 1
 SQ SEQUENCE 485 AA; 55733 MW; B90456AC53393CB2 CRC64;

 Query Match 51.0%; Score 78; DB 2; Length 485;
 Best Local Similarity 51.6%; Pred. No. 0.04;
 Matches 16; Conservative 7; Mismatches 8; Indels 0; Gaps 0;

 Qy 1 KEARKVSRGIDRMLRDKRDLQOQTHRLLLLG 31
 Db 13 REARKVKNQIEQLAKDKQVWRATHRLLLLG 43


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Query Match      49.7%  Score 76;  DB 1;  Length 353;
Best Local Similarity 51.6%  Pred. No. 0.055;
Matches 16;  Conservative 7;  Mismatches 8;  Indels 0;  Gaps 0;

QY  1 KEARKVSRGIDRMLRDQKRLQOQTHRLLLLG 31
    |||||:::|||||:::|||
Db. 10 KEARRINDEIERQLRRDKRDARRELKLLLG 40
    |||||:::|||||:::|||

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RESULT 12
GNAQ_MOUSE STANDARD; PRT; 353 AA.
ID P21279; Q69PF5;
DT 01-MAY-1991 (Rel. 18, Created)
DT 01-FEB-2005 (Rel. 46, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Guanine nucleotide-binding protein G(q), alpha subunit.
GN Name=Gnaq;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Muridae; Murinae; Mus.
OC NCBI_TaxID=10090;
RN [1]
NN NUCLEOTIDE SEQUENCE.
RP TISSUE=Brain;
RX MEDLINE=91067657; PubMed=2123549;
RN Strachmann M., Simon M.I.;
RT "G protein diversity: a distinct class of alpha subunits is present in
RL vertebrates and invertebrates.";
RN Proc. Natl. Acad. Sci. U.S.A. 87:9113-9117(1990).
RN [2]
NN NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
RP STRAIN=C57BL/6; TISSUE=Brain;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RN Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Donald M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Morley D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnurch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RN and mouse cDNA sequences.";
RN Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [3]
NN PALMITOYLATION.
RP TISSUE=Brain;
RX MEDLINE=94043367; PubMed=8227063;
RN Wedegaertner P.B., Chu D.H., Wilson P.T., Lewis M.J., Bourne H.R.;
RT "Palmitoylation is required for signaling functions and membrane
RN attachment of Gq alpha and Gs alpha.";
RL J. Biol. Chem. 268:25001-25008(1993).
CC CC -1- FUNCTION: Guanine nucleotide-binding proteins (G proteins) are
CC involved as modulators or transducers in various transmembrane
CC signaling systems.
CC CC -1- SUBUNIT: G proteins are composed of 3 units; alpha, beta and
CC gamma. The alpha chain contains the guanine nucleotide binding
CC site. Binds SIC9A3R1 (By similarity).
CC CC -1- SIMILARITY: Belongs to the G-alpha family, G(q) subfamily.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
DR ENBL; M55412; AAA63306.1; ALT INIT; mRNA.
DR ENBL; BC057583; AAH57583.1; ALT_INIT; mRNA.
DR PIR; A38414; RGMQ5.
DR HSPSP; P04896; 1CUJ.
DR Ensembl; ENSMUSG00000024639; Mus musculus.

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SQ SEQUENCE 359 AA; 42142 MW; 6F69C4F617DFA7C7 CRC64;

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Best Local Similarity 51.6%; Pred. No. 0.056;
Matches 16; Conservative 7; Mismatches 8; Indels 0; Gaps 0;

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Db       16 KEARRINDEIERQLRRDKEDARRELKLLILG 46

RESULT 15
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AC QSF3B5;
DT 10-MAY-2005 (T=EMBLrel. 30, Created)
DT 10-MAY-2005 (T=EMBLrel. 30, Last sequence update)
DE Hypothetical protein.
GN ORPNames=RCJMB04_23b22;
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA STRAIN=CB; TISSUE=Bursa;
RC Caldwell R.B., Kierzek A.M., Arakawa H., Bezzubov Y., Zaim J.,
RA Fiedler P., Kutter S., Blagodatski A., Kostovska D., Kotter M.,
RA Plachy J., Carninci P., Hayashizaki Y., Buerstedde J.M.;
RT "Full-length cDNAs from chicken bursal lymphocytes to facilitate
RT gene function analysis."
RL Genome Biol. 6:R6-R6(2005).
DR ENML; AJ851735; CAH6S369.1; -; mRNA.
DR InterPro; IPR011025; GproteinA_insert.
DR InterPro; IPR001019; Gprotein_alpha.
DR InterPro; IPR000654; Gprotein_alpha_Q.
DR Pfam; PF00503; G-alpha; 1.
DR PRINTS; PR00318; GPROTEINA.
DR PRINTS; PR00442; GPROTEINAQ.
DR ProDom; PD000281; Gprotein_alpha; 1.
DR SMART; SM00275; G_alpha; 1.
KW Hypothetical protein.
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Query Match          49.7%; Score 76; DB 2; Length 359;
Best Local Similarity 51.6%; Pred. No. 0.056;
Matches 16; Conservative 7; Mismatches 8; Indels 0; Gaps 0;

QY      1 KEARKVSRGIDRMRLRDKRDQLQOTHRLLILG 31
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Db       16 KEARRINDEIERQLRRDKEDARRELKLLILG 46

Search completed: March 2, 2006, 19:37:30
Job time : 21.3988 secs

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2	76	49.7	353	2	US-09-984-292-4	Sequence 4, Appli
3	76	49.7	353	2	US-09-984-292-5	Sequence 5, Appli
4	76	49.7	353	2	US-09-984-292-16	Sequence 16, Appl
5	76	49.7	359	2	US-09-984-293-1	Sequence 1, Appli
6	76	49.7	359	2	US-09-984-293-3	Sequence 3, Appli
7	76	49.7	359	2	US-09-984-293-10	Sequence 10, Appl
8	76	49.7	359	2	US-09-984-292-15	Sequence 15, Appl
9	76	49.7	359	2	US-09-984-292-20	Sequence 20, Appl
10	76	49.7	359	2	US-09-984-293-37	Sequence 37, Appl
11	71	46.4	353	2	US-09-984-293-6	Sequence 6, Appli
12	71	46.4	353	2	US-09-984-293-8	Sequence 8, Appli
13	71	46.4	353	2	US-09-984-292-14	Sequence 14, Appl
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15	71	46.4	353	2	US-09-984-292-18	Sequence 18, Appl
16	71	46.4	353	2	US-09-984-293-19	Sequence 19, Appl
17	71	46.4	353	2	US-09-984-293-24	Sequence 24, Appl
18	71	46.4	357	2	US-09-984-293-7	Sequence 7, Appli
19	71	46.4	359	2	US-09-984-293-9	Sequence 9, Appli
20	71	46.4	359	2	US-09-984-293-11	Sequence 11, Appl
21	71	46.4	359	2	US-09-984-293-12	Sequence 12, Appl
22	71	46.4	359	2	US-09-984-293-13	Sequence 13, Appl
23	71	46.4	359	2	US-09-984-293-21	Sequence 21, Appl
24	71	46.4	359	2	US-09-984-292-22	Sequence 22, Appl
25	71	46.4	359	2	US-09-984-292-23	Sequence 23, Appl
26	71	46.4	359	2	US-09-984-293-25	Sequence 25, Appl
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; LENGTH: 353
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 ; ORGANISM: M
 US-09-984-292-4

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Best Local Similarity 51.6%; Pred. No. 0.0012;
Matches 16; Conservative 7; Mismatches 8; Indels

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Db 10 KEARRINDEIERQLRRDRKRDARRELKLLLLG 40

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US-09-984-292-5
; Sequence 5, Application US/09984292
; Patent No. 6818747
; GENERAL INFORMATION:
; APPLICANT: YAO, YONG
; APPLICANT: XU, HONG
; TITLE OF INVENTION: G-ALPHA-Q PROT
; TITLE OF INVENTION: ANALYSIS AND
; TITLE OF INVENTION: CHEMOSENSORY
; FILE REFERENCE: 078003-0280649
; CURRENT APPLICATION NUMBER: US/09/
; CURRENT FILING DATE: 2001-10-29
; PRIOR APPLICATION NUMBER: 60/243,7
; PRIOR FILING DATE: 2000-10-30
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 353
; TYPE: PRT
; ORGANISM: Mus sp.
US-09-984-292-5

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Query Match 49.7%; Score 76; DB 2; Length 353;
Best Local Similarity 51.6%; Pred. No. 0.0012;
Matches 16; Conservative 7; Mismatches 8; Indels

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D_b	10 KEARRINDEIERQLRRDKRDARRELKLLLG 40 :: : :::

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; Patent No. 6818747
; GENERAL INFORMATION:
; APPLICANT: YAO, YONG
; APPLICANT: XU, HONG
; TITLE OF INVENTION: G-ALPHA-Q PROTEIN VARIANTS AND THEIR USE IN THE
; TITLE OF INVENTION: ANALYSIS AND DISCOVERY OF AGONISTS AND ANTAGONISTS OF
; TITLE OF INVENTION: CHEMOSENSORY RECEPTORS
; FILE REFERENCE: 078003-0280649
; CURRENT APPLICATION NUMBER: US/09/984,292
; CURRENT FILING DATE: 2001-10-29
; PRIOR APPLICATION NUMBER: 60/243,770
; PRIOR FILING DATE: 2000-10-30
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 16
; LENGTH: 353
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-984-292-16

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Query Match 49.7%; Score 76; DB 2; Length 353;
Best Local Similarity 51.6%; Pred.No. 0.0012;
Matches 16; Conservative 7; Mismatches 8; Indels

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|||||:: | : | | ||| :: : |||||

Db 10 KEARRINDEIERQLRRDKRDARRELKLLLG 40

RESULT 5
 US-09-984-292-1
 ; Sequence 1, Application US/09984292
 ; Patent No. 6818747
 ; GENERAL INFORMATION:
 ; APPLICANT: YAO, YONG
 ; APPLICANT: XU, HONG
 ; TITLE OF INVENTION: G-ALPHA-Q PROTEIN VARIANTS AND THEIR USE IN THE
 ; TITLE OF INVENTION: ANALYSIS AND DISCOVERY OF AGONISTS AND ANTAGONISTS OF
 ; TITLE OF INVENTION: CHEMOSENSORY RECEPTORS
 ; FILE REFERENCE: 078003-0280649
 ; CURRENT APPLICATION NUMBER: US/09/984,292
 ; CURRENT FILING DATE: 2001-10-29
 ; PRIOR APPLICATION NUMBER: 60/243,770
 ; PRIOR FILING DATE: 2000-10-30
 ; NUMBER OF SEQ ID NOS: 42
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 1
 ; LENGTH: 359
 ; TYPE: PRT
 ; ORGANISM: Mus sp.
 US-09-984-292-1

Query Match 49.7%; Score 76; DB 2; Length 359;
Best Local Similarity 51.6%; Pred. No. 0.0012;
Matches 16; Conservative 7; Mismatches 8; Gaps 0;

QY 1 KEARKVSGIDRWLRDQKRDLOQTHRLLLG 31
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16 KEARRNDEIEROLRRDKRDARELKLLLG 46

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RESULT 6
US-09-984-292-3
; Sequence 3, Application US/09984292
; Patent No. 6818747
; GENERAL INFORMATION:
; APPLICANT: YAO, YONG
; APPLICANT: XU, HONG
; TITLE OF INVENTION: G-ALPHA-Q PROTEIN
; TITLE OF INVENTION: ANALYSIS AND
; TITLE OF INVENTION: CHEMOSENSORY
; FILE REFERENCES: 078003-0280649
; CURRENT APPLICATION NUMBER: US/09/
; CURRENT FILING DATE: 2001-10-29
; PRIOR APPLICATION NUMBER: 60/243,7
; PRIOR FILING DATE: 2000-10-30
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; ORGANISM: Mus sp.
US-09-984-292-3

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Best Local Similarity	51.6%;	Pred. No. 0.0012;		
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RESULT 7
US-09-984-292-10
; Sequence 10, Application US/09984292
; Patent No 6818747

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; GENERAL INFORMATION:
; APPLICANT: YAO, YONG
; TITLE OF INVENTION: G-ALPHA-Q PROTEIN VARIANTS AND THEIR USE IN THE
; TITLE OF INVENTION: ANALYSIS AND DISCOVERY OF AGONISTS AND ANTAGONISTS OF
; TITLE OF INVENTION: CHEMOSENSORY RECEPTORS
; FILE REFERENCE: 078003-0280649
; CURRENT APPLICATION NUMBER: US/09/984,292
; PRIOR FILING DATE: 2001-10-29
; PRIOR FILING DATE: 2001-10-29
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 10
; LENGTH: 359
; TYPE: PRT
; ORGANISM: Mus sp.
US-09-984-292-10

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RESULT 8
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; Sequence 15, Application US/09984292
; Patent No. 6818747
; GENERAL INFORMATION:
; APPLICANT: YAO, YONG
; APPLICANT: XU, HONG
; TITLE OF INVENTION: G-ALPHA-Q PROTEIN VARIANTS AND THEIR USE IN THE
; TITLE OF INVENTION: ANALYSIS AND DISCOVERY OF AGONISTS AND ANTAGONISTS OF
; TITLE OF INVENTION: CHEMOSENSORY RECEPTORS
; FILE REFERENCE: 078003-0280649
; CURRENT APPLICATION NUMBER: US/09/984,292
; CURRENT FILING DATE: 2001-10-29
; PRIOR FILING DATE: 2001-10-29
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 15
; LENGTH: 359
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-984-292-15

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RESULT 9
US-09-984-292-20
; Sequence 20, Application US/09984292
; Patent No. 6818747
; GENERAL INFORMATION:
; APPLICANT: YAO, YONG
; APPLICANT: XU, HONG
; TITLE OF INVENTION: G-ALPHA-Q PROTEIN VARIANTS AND THEIR USE IN THE
; TITLE OF INVENTION: ANALYSIS AND DISCOVERY OF AGONISTS AND ANTAGONISTS OF
; TITLE OF INVENTION: CHEMOSENSORY RECEPTORS
; FILE REFERENCE: 078003-0280649
; CURRENT APPLICATION NUMBER: US/09/984,292
; CURRENT FILING DATE: 2001-10-29
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; PRIOR APPLICATION NUMBER: 60/243,770
; PRIOR FILING DATE: 2000-10-30
; NUMBER OF SEQ ID NOS: 42
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; SEQ ID NO 20
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; ORGANISM: Homo sapiens
US-09-984-292-20

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Best Local Similarity 51.6%; Pred. No. 0.0012;
Matches 16; Conservative 7; Mismatches 8; Indels 0; Gaps 0;

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RESULT 10
US-09-984-292-37
; Sequence 37, Application US/09984292
; Patent No. 6818747
; GENERAL INFORMATION:
; APPLICANT: YAO, YONG
; APPLICANT: XU, HONG
; TITLE OF INVENTION: G-ALPHA-Q PROTEIN VARIANTS AND THEIR USE IN THE
; TITLE OF INVENTION: ANALYSIS AND DISCOVERY OF AGONISTS AND ANTAGONISTS OF
; TITLE OF INVENTION: CHEMOSENSORY RECEPTORS
; FILE REFERENCE: 078003-0280649
; CURRENT APPLICATION NUMBER: US/09/984,292
; CURRENT FILING DATE: 2001-10-29
; PRIOR FILING DATE: 2001-10-29
; PRIOR FILING DATE: 2000-10-30
; NUMBER OF SEQ ID NOS: 42
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; SEQ ID NO 37
; LENGTH: 359
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-984-292-37

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Db      16 KEARRINDEIERQLRRDKRDARRELKLLIG 46

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; Sequence 6, Application US/09984292
; Patent No. 6818747
; GENERAL INFORMATION:
; APPLICANT: YAO, YONG
; APPLICANT: XU, HONG
; TITLE OF INVENTION: G-ALPHA-Q PROTEIN VARIANTS AND THEIR USE IN THE
; TITLE OF INVENTION: ANALYSIS AND DISCOVERY OF AGONISTS AND ANTAGONISTS OF
; TITLE OF INVENTION: CHEMOSENSORY RECEPTORS
; FILE REFERENCE: 078003-0280649
; CURRENT APPLICATION NUMBER: US/09/984,292
; CURRENT FILING DATE: 2001-10-29
; PRIOR FILING DATE: 2001-10-29
; PRIOR FILING DATE: 2000-10-30
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; SEQ ID NO 6
; LENGTH: 353
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; ORGANISM: Mus sp.
US-09-984-292-6
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GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: March 2, 2006, 19:32:31 ; Search time 14.137 Seconds
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Title: US-10-618-320A-1_COPY_96_126

Perfect score: 153

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Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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4	95	62.1	351	5	US-10-732-923-8014
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6	79	51.6	378	5	US-10-732-923-7865
7	79	51.6	385	4	US-10-369-493-4978
8	79	51.6	385	5	US-10-732-923-7867
9	76	49.7	353	3	US-09-984-292-2
10	76	49.7	353	3	US-09-984-292-4
11	76	49.7	353	3	US-09-984-292-5
12	76	49.7	353	3	US-09-984-292-16
13	76	49.7	353	3	US-09-989-497-2
14	76	49.7	353	3	US-09-989-497-4
15	76	49.7	353	3	US-09-989-497-5
16	76	49.7	353	3	US-09-989-497-16
17	76	49.7	353	3	US-09-952-680A-27
18	76	49.7	353	4	US-10-352-843-13
19	76	49.7	353	5	US-10-215-982-27
20	76	49.7	353	5	US-10-732-923-7646
21	76	49.7	353	5	US-10-732-923-7999
22	76	49.7	353	5	US-10-732-923-8036
23	76	49.7	353	5	US-10-931-080B-5
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32 76 49.7 359 3 US-09-984-292-37
33 76 49.7 359 3 US-09-989-497-1
34 76 49.7 359 3 US-09-989-497-3
35 76 49.7 359 3 US-09-989-497-10
36 76 49.7 359 3 US-09-989-497-15
37 76 49.7 359 3 US-09-989-497-20
38 76 49.7 359 3 US-09-989-497-37
39 76 49.7 359 4 US-10-059-266B-2
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42 76 49.7 359 5 US-10-732-923-7995
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45 76 49.7 359 5 US-10-732-923-8037

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Sequence 10, Appl
Sequence 15, Appl
Sequence 20, Appl
Sequence 37, Appl
Sequence 1, Appli
Sequence 2, Appli
Sequence 10, Appl
Sequence 15, Appl
Sequence 20, Appl
Sequence 37, Appl
Sequence 7647, Ap
Sequence 7961, Ap
Sequence 7995, Ap
Sequence 8000, Ap
Sequence 8002, Ap
Sequence 8037, Ap

ALIGNMENTS

RESULT 1
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; Publication No. US20050108791A1
; GENERAL INFORMATION:
; APPLICANT: Edgerton, Michael D
; TITLE OF INVENTION: TRANSGENIC PLANTS WITH IMPROVED PHENOTYPES
; FILE REFERENCE: 38-15(52796)C
; CURRENT APPLICATION NUMBER: US/10/732,923
; CURRENT FILING DATE: 2003-12-10
; PRIOR APPLICATION NUMBER: 10/310,154
; PRIOR FILING DATE: 2002-12-04
; NUMBER OF SEQ ID NOS: 24149
; SEQ ID NO 8011
; LENGTH: 458
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-732-923-8011

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Best Local Similarity 100.0%; Pred. No. 6.4e-13;
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; Publication No. US20050196754A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc
; TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
; FILE REFERENCE: 790CIP3/US
; CURRENT APPLICATION NUMBER: US/10/450,763
; CURRENT FILING DATE: 2003-06-11
; PRIOR APPLICATION NUMBER: PCT/US01/08631
; PRIOR FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: 09/540,217
; PRIOR FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: 09/649,167
; PRIOR FILING DATE: 2000-08-23
; NUMBER OF SEQ ID NOS: 60736
; SOFTWARE: Custom
; SEQ ID NO 31595
; LENGTH: 461
; TYPE: PRT
; ORGANISM: Homo sapiens


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; CURRENT FILING DATE: 2001-10-29
; PRIOR APPLICATION NUMBER: 60/243,770
; PRIOR FILING DATE: 2000-10-30
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 16
; LENGTH: 353
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-984-292-16

Query Match          49.7%; Score 76; DB 3; Length 353;
Best Local Similarity 51.6%; Pred. No. 0.029;
Matches 16; Conservative 7; Mismatches 8; Indels 0; Gaps 0;

QY 1 KEARKVSRGIDRLMDQKRDQLQOQTHRLLLG 31
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Db 10 KEARRINDEIERQLRRDKRDARRELKLLLG 40

RESULT 13
US-09-989-497-2
; Sequence 2, Application US/09989497
; Patent No. US20020143151A1
; GENERAL INFORMATION:
; APPLICANT: YAO, YONG
; APPLICANT: XU, HONG
; TITLE OF INVENTION: G-ALPHA-Q PROTEIN VARIANTS AND THEIR USE IN THE
; TITLE OF INVENTION: ANALYSIS AND DISCOVERY OF AGONISTS AND ANTAGONISTS OF
; TITLE OF INVENTION: CHEMOSENSORY RECEPTORS
; FILE REFERENCE: 078003-0280735
; CURRENT APPLICATION NUMBER: US/09/989,497
; CURRENT FILING DATE: 2001-11-21
; PRIOR APPLICATION NUMBER: 09/984,292
; PRIOR FILING DATE: 2001-10-29
; PRIOR APPLICATION NUMBER: 60/243,770
; PRIOR FILING DATE: 2000-10-30
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 353
; TYPE: PRT
; ORGANISM: Mus sp.
US-09-989-497-2

Query Match          49.7%; Score 76; DB 3; Length 353;
Best Local Similarity 51.6%; Pred. No. 0.029;
Matches 16; Conservative 7; Mismatches 8; Indels 0; Gaps 0;

QY 1 KEARKVSRGIDRLMDQKRDQLQOQTHRLLLG 31
    |||||:::|:|:| |||||:::|:|:|
Db 10 KEARRINDEIERQLRRDKRDARRELKLLLG 40

RESULT 14
US-09-989-497-4
; Sequence 4, Application US/09989497
; Patent No. US20020143151A1
; GENERAL INFORMATION:
; APPLICANT: YAO, YONG
; APPLICANT: XU, HONG
; TITLE OF INVENTION: G-ALPHA-Q PROTEIN VARIANTS AND THEIR USE IN THE
; TITLE OF INVENTION: ANALYSIS AND DISCOVERY OF AGONISTS AND ANTAGONISTS OF
; TITLE OF INVENTION: CHEMOSENSORY RECEPTORS
; FILE REFERENCE: 078003-0280735
; CURRENT APPLICATION NUMBER: US/09/989,497
; CURRENT FILING DATE: 2001-11-21
; PRIOR APPLICATION NUMBER: 09/984,292
; PRIOR FILING DATE: 2001-10-29
; PRIOR APPLICATION NUMBER: 60/243,770
; PRIOR FILING DATE: 2000-10-30
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn Ver. 2.1
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; SEQ ID NO 4
; LENGTH: 353
; TYPE: PRT
; ORGANISM: Mus sp.
US-09-989-497-4

Query Match          49.7%; Score 76; DB 3; Length 353;
Best Local Similarity 51.6%; Pred. No. 0.029;
Matches 16; Conservative 7; Mismatches 8; Indels 0; Gaps 0;

QY 1 KEARKVSRGIDRLMDQKRDQLQOQTHRLLLG 31
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Db 10 KEARRINDEIERQLRRDKRDARRELKLLLG 40

RESULT 15
US-09-989-497-5
; Sequence 5, Application US/09989497
; Patent No. US20020143151A1
; GENERAL INFORMATION:
; APPLICANT: YAO, YONG
; APPLICANT: XU, HONG
; TITLE OF INVENTION: G-ALPHA-Q PROTEIN VARIANTS AND THEIR USE IN THE
; TITLE OF INVENTION: ANALYSIS AND DISCOVERY OF AGONISTS AND ANTAGONISTS OF
; TITLE OF INVENTION: CHEMOSENSORY RECEPTORS
; FILE REFERENCE: 078003-0280735
; CURRENT APPLICATION NUMBER: US/09/989,497
; CURRENT FILING DATE: 2001-11-21
; PRIOR APPLICATION NUMBER: 09/984,292
; PRIOR FILING DATE: 2001-10-29
; PRIOR APPLICATION NUMBER: 60/243,770
; PRIOR FILING DATE: 2000-10-30
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 353
; TYPE: PRT
; ORGANISM: Mus sp.
US-09-989-497-5

Query Match          49.7%; Score 76; DB 3; Length 353;
Best Local Similarity 51.6%; Pred. No. 0.029;
Matches 16; Conservative 7; Mismatches 8; Indels 0; Gaps 0;

QY 1 KEARKVSRGIDRLMDQKRDQLQOQTHRLLLG 31
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Db 10 KEARRINDEIERQLRRDKRDARRELKLLLG 40

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Job time : 14.137 secs
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GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: March 2, 2006, 19:37:27 ; Search time 1.07771 Seconds
(without alignments)
575.298 Million cell updates/sec

Title: US-10-618-320A-1_COPY_96_126

Perfect score: 153

Sequence: 1 KEARKVSRGIDRMRLDKEDLQOTHRLLLLG 31

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 135339 seqs, 20000136 residues

Total number of hits satisfying chosen parameters: 135339

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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8: /cgn2_6/prodata/2/pubpaa/US60_NEW_PUB.pap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	153	100.0	458	6	US-10-618-320A-1
2	149	97.4	448	6	US-10-618-320A-25
3	149	97.4	450	6	US-10-618-320A-26
4	76	49.7	859	7	US-11-053-100-52
5	76	49.7	1309	7	US-11-053-100-53
6	71	46.4	353	7	US-11-060-023-2
7	71	46.4	353	7	US-11-060-023-4
8	71	46.4	353	7	US-11-060-023-6
9	71	46.4	353	7	US-11-060-023-8
10	71	46.4	353	7	US-11-060-023-12
11	71	46.4	353	7	US-11-060-023-14
12	71	46.4	353	7	US-11-060-023-16
13	71	46.4	359	7	US-11-060-023-11
14	71	46.4	359	7	US-11-060-023-13
15	71	46.4	360	7	US-11-060-023-17
16	68	44.4	353	7	US-11-060-023-15
17	64	41.8	394	6	US-10-821-234-1626
18	64	41.8	864	7	US-11-053-100-58
19	58	37.9	374	7	US-11-228-364-4
20	54	35.3	374	7	US-11-060-023-10
21	54	35.3	374	7	US-11-228-364-2
22	54	35.3	374	7	US-11-169-041-188
23	53	34.6	641	6	US-10-821-234-1519
24	53	34.6	641	6	US-10-491-096-189
25	51	33.3	646	6	US-10-491-096-190

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26 49 32.0 337 7 US-11-087-099-6276 Sequence 6276, Ap
27 46 30.1 452 7 US-11-024-959-382 Sequence 382, App
28 45 29.4 408 6 US-10-821-234-1100 Sequence 1100, Ap
29 45 29.4 411 7 US-11-072-512-3452 Sequence 3452, Ap
30 45 29.4 763 6 US-10-821-234-1619 Sequence 1619, Ap
31 45 29.4 915 6 US-10-821-234-1514 Sequence 1514, Ap
32 45 29.4 915 6 US-10-995-561-1003 Sequence 1003, Ap
33 45 29.4 917 6 US-10-995-561-1000 Sequence 1000, Ap
34 45 29.4 940 6 US-10-995-561-1004 Sequence 1004, Ap
35 45 29.4 969 6 US-10-995-561-1001 Sequence 1001, Ap
36 45 29.4 971 6 US-10-995-561-998 Sequence 998, App
37 45 29.4 994 6 US-10-995-561-997 Sequence 997, App
38 44.5 29.1 299 6 US-10-362-772-2 Sequence 2, Appli
39 44 28.8 250 6 US-10-453-372-938 Sequence 938, App
40 44 28.8 452 7 US-11-024-959-451 Sequence 451, App
41 44 28.8 625 7 US-11-072-512-3210 Sequence 3210, Ap
42 44 28.8 2087 7 US-11-075-185-28 Sequence 28, Appl
43 43.5 28.4 250 7 US-11-087-099-8190 Sequence 8190, Ap
44 43 28.1 246 7 US-11-232-406A-14 Sequence 14, Appl
45 43 28.1 250 6 US-10-453-372-942 Sequence 942, App

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ALIGNMENTS

RESULT 1

US-10-618-320A-1

; Sequence 1, Application US/10618320A

; Publication No. US20050260595A1

; GENERAL INFORMATION:

; APPLICANT: Sumitomo Chemical Company Limited

; TITLE OF INVENTION: NOVEL G PROTEINS, POLYNUCLEOTIDE ENCODING THE SAME AND UTILIZATION

; FILE REFERENCE:

; CURRENT APPLICATION NUMBER: US/10/618,320A

; PRIOR FILING DATE: 2003-07-11

; PRIOR APPLICATION NUMBER: JP 2002/206841

; PRIOR FILING DATE: 2002-07-16

; PRIOR APPLICATION NUMBER: JP 2002/367778

; PRIOR FILING DATE: 2002-12-19

; PRIOR APPLICATION NUMBER: JP 2003/095955

; PRIOR FILING DATE: 2003-03-31

; NUMBER OF SEQ ID NOS: 34

; SEQ ID NO 1

; LENGTH: 458

; TYPE: PRT

; ORGANISM: Homo sapiens

; US-10-618-320A-1

Query Match 100.0%; Score 153; DB 6; Length 458;

Best Local Similarity 100.0%; Pred. No. 68-15;

Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KEARKVSRGIDRMRLDKEDLQOTHRLLLLG 31

DB 96 KEARKVSRGIDRMRLDKEDLQOTHRLLLLG 126

RESULT 2

US-10-618-320A-25

; Sequence 25, Application US/10618320A

; Publication No. US20050260595A1

; GENERAL INFORMATION:

; APPLICANT: Sumitomo Chemical Company Limited

; TITLE OF INVENTION: NOVEL G PROTEINS, POLYNUCLEOTIDE ENCODING THE SAME AND UTILIZATION

; FILE REFERENCE:

; CURRENT APPLICATION NUMBER: US/10/618,320A

; PRIOR FILING DATE: 2003-07-11

; PRIOR APPLICATION NUMBER: JP 2002/206841

; PRIOR FILING DATE: 2002-07-16

; PRIOR APPLICATION NUMBER: JP 2002/367778

; PRIOR FILING DATE: 2002-12-19

; PRIOR APPLICATION NUMBER: JP 2003/095955

; PRIOR FILING DATE: 2003-03-31

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/ NUMBER OF SEQ ID NOS: 34
/ SEQ ID NO 25
/ LENGTH: 448
/ TYPE: PRT
/ ORGANISM: Mus musculus
US-10-618-320A-25

Query Match          97.4%; Score 149; DB 6; Length 448;
Best Local Similarity 96.8%; Pred. No. 2.3e-14;
Matches 30; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KEARKVSRGIDRMRLRDQKRDQLQOQTHRLLLG 31
Db 86 KEARKVSRGIDRMRLRDQKRDQLQOQTHRLLLG 116

RESULT 3
US-10-618-320A-26
/ Sequence 26, Application US/10618320A
/ Publication No. US20050260595A1
/ GENERAL INFORMATION:
/ APPLICANT: Sumitomo Chemical Company Limited
/ TITLE OF INVENTION: NOVEL G PROTEINS, POLYNUCLEOTIDE ENCODING THE SAME AND UTILIZATION
/ FILE REFERENCE:
/ CURRENT APPLICATION NUMBER: US/10/618,320A
/ PRIOR FILING DATE: 2003-07-11
/ PRIOR APPLICATION NUMBER: JP 2002/206841
/ PRIOR FILING DATE: 2002-07-16
/ PRIOR APPLICATION NUMBER: JP 2002/367778
/ PRIOR FILING DATE: 2002-12-19
/ PRIOR APPLICATION NUMBER: JP 2003/095955
/ PRIOR FILING DATE: 2003-03-31
/ NUMBER OF SEQ ID NOS: 34
/ SEQ ID NO 26
/ LENGTH: 450
/ TYPE: PRT
/ ORGANISM: Rattus norvegicus
US-10-618-320A-26

Query Match          97.4%; Score 149; DB 6; Length 450;
Best Local Similarity 96.8%; Pred. No. 2.3e-14;
Matches 30; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KEARKVSRGIDRMRLRDQKRDQLQOQTHRLLLG 31
Db 88 KEARKVSRGIDRMRLRDQKRDQLQOQTHRLLLG 118

RESULT 4
US-11-053-100-52
/ Sequence 52, Application US/11053100
/ Publication No. US2005025554A1
/ GENERAL INFORMATION:
/ APPLICANT: CHILKOTI, Ashutosh
/ TITLE OF INVENTION: FUSION PEPTIDES ISOLATABLE BY PHASE TRANSITION
/ FILE REFERENCE: 4176-101 CIP
/ CURRENT APPLICATION NUMBER: US/11/053,100
/ CURRENT FILING DATE: 2005-02-08
/ PRIOR APPLICATION NUMBER: US 09/812,382
/ PRIOR FILING DATE: 2001-03-20
/ PRIOR APPLICATION NUMBER: US 60/190,659
/ PRIOR FILING DATE: 2000-03-20
/ NUMBER OF SEQ ID NOS: 58
/ SOFTWARE: PatentIn version 3.3
/ SEQ ID NO 52
/ LENGTH: 859
/ TYPE: PRT
/ ORGANISM: Artificial
/ FEATURE:
/ OTHER INFORMATION: Synthetic Construct
/ NAME/KEY: MISC FEATURE
/ LOCATION: (1)..(859)

Query Match          97.4%; Score 149; DB 6; Length 450;
Best Local Similarity 96.8%; Pred. No. 2.3e-14;
Matches 30; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KEARKVSRGIDRMRLRDQKRDQLQOQTHRLLLG 31
Db 88 KEARKVSRGIDRMRLRDQKRDQLQOQTHRLLLG 118
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/ OTHER INFORMATION: pET15b-SD1-ELP1-90-throm-G protein alpha Q
US-11-053-100-52

Query Match          49.7%; Score 76; DB 7; Length 859;
Best Local Similarity 51.6%; Pred. No. 0.0026;
Matches 16; Conservative 7; Mismatches 8; Indels 0; Gaps 0;

QY 1 KEARKVSRGIDRMRLRDQKRDQLQOQTHRLLLG 31
Db 516 KEARRINDEIERQLRRDKRDARRELKLLLLG 546

RESULT 5
US-11-053-100-53
/ Sequence 53, Application US/11053100
/ Publication No. US2005025554A1
/ GENERAL INFORMATION:
/ APPLICANT: CHILKOTI, Ashutosh
/ TITLE OF INVENTION: FUSION PEPTIDES ISOLATABLE BY PHASE TRANSITION
/ FILE REFERENCE: 4176-101 CIP
/ CURRENT APPLICATION NUMBER: US/11/053,100
/ CURRENT FILING DATE: 2005-02-08
/ PRIOR APPLICATION NUMBER: US 09/812,382
/ PRIOR FILING DATE: 2001-03-20
/ PRIOR APPLICATION NUMBER: US 60/190,659
/ PRIOR FILING DATE: 2000-03-20
/ NUMBER OF SEQ ID NOS: 58
/ SOFTWARE: PatentIn version 3.3
/ SEQ ID NO 53
/ LENGTH: 1309
/ TYPE: PRT
/ ORGANISM: Artificial
/ FEATURE:
/ OTHER INFORMATION: Synthetic Construct
/ NAME/KEY: MISC FEATURE
/ LOCATION: (1)..(1309)
/ OTHER INFORMATION: pET15b-SD1-ELP1-180-throm-G protein alpha Q
US-11-053-100-53

Query Match          49.7%; Score 76; DB 7; Length 1309;
Best Local Similarity 51.6%; Pred. No. 0.0043;
Matches 16; Conservative 7; Mismatches 8; Indels 0; Gaps 0;

QY 1 KEARKVSRGIDRMRLRDQKRDQLQOQTHRLLLG 31
Db 966 KEARRINDEIERQLRRDKRDARRELKLLLLG 996

RESULT 6
US-11-060-023-2
/ Sequence 2, Application US/11060023
/ Publication No. US20050255531A1
/ GENERAL INFORMATION:
/ APPLICANT: Aventis Pharma Deutschland GmbH
/ TITLE OF INVENTION: Process for identifying modulators of G protein coupled
/ FILE REFERENCE: AVE D-2000/A033 englisch
/ CURRENT APPLICATION NUMBER: US/11/060,023
/ CURRENT FILING DATE: 2005-02-17
/ PRIOR APPLICATION NUMBER: US/09/899,295
/ PRIOR FILING DATE: 2003-07-06
/ NUMBER OF SEQ ID NOS: 17
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 2
/ LENGTH: 353
/ TYPE: PRT
/ ORGANISM: Mus musculus
US-11-060-023-2

Query Match          46.4%; Score 71; DB 7; Length 353;
Best Local Similarity 48.4%; Pred. No. 0.0047;
Matches 15; Conservative 8; Mismatches 8; Indels 0; Gaps 0;
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; GENERAL INFORMATION:
; APPLICANT: Aventis Pharma Deutschland GmbH
; TYPE: PRT
; ORGANISM: Mus musculus
; TITLE OF INVENTION: Process for identifying modulators of G protein coupled
US-11-060-023-14

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; Publication No. US20050255531A1
; GENERAL INFORMATION:
; APPLICANT: Aventis Pharma Deutschland GmbH
; TITLE OF INVENTION: Process for identifying modulators of G protein coupled
; TITLE OF INVENTION: receptors
; FILE REFERENCE: AVE D-2000/A033 englisch
; CURRENT APPLICATION NUMBER: US/11/060,023
; CURRENT FILING DATE: 2005-02-17
; PRIOR APPLICATION NUMBER: US/09/899,295
; PRIOR FILING DATE: 2003-07-06
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 13
; LENGTH: 359
; TYPE: PRT
; ORGANISM: Mus musculus
; US-11-060-023-13

Query Match 46.4%; Score 71; DB 7; Length 359;
Best Local Similarity 48.4%; Pred. No. 0.0048;
Matches 15; Conservative 8; Mismatches 8; Indels 0; Gaps 0;

QY 1 KEARKVSRGIDRMLRDQKRDLOQTHRLLLLG 31
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DB 10 KEARRINDEIERHVRDKRDARRELKLLLG 40
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RESULT 12
US-11-060-023-16
; Sequence 16, Application US/11060023
; Publication No. US20050255531A1
; GENERAL INFORMATION:
; APPLICANT: Aventis Pharma Deutschland GmbH
; TITLE OF INVENTION: Process for identifying modulators of G protein coupled
; TITLE OF INVENTION: receptors
; FILE REFERENCE: AVE D-2000/A033 englisch
; CURRENT APPLICATION NUMBER: US/11/060,023
; CURRENT FILING DATE: 2005-02-17
; PRIOR APPLICATION NUMBER: US/09/899,295
; PRIOR FILING DATE: 2003-07-06
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 16
; LENGTH: 353
; TYPE: PRT
; ORGANISM: Mus musculus
; US-11-060-023-16

Query Match 46.4%; Score 71; DB 7; Length 353;
Best Local Similarity 48.4%; Pred. No. 0.0047;
Matches 15; Conservative 8; Mismatches 8; Indels 0; Gaps 0;

QY 1 KEARKVSRGIDRMLRDQKRDLOQTHRLLLLG 31
    |||::: |:|:| |||::: |||
DB 10 KEARRINDEIERHVRDKRDARRELKLLLG 40
    |||::: |:|:| |||::: |||

RESULT 13
US-11-060-023-11
; Sequence 11, Application US/11060023
; Publication No. US20050255531A1
; GENERAL INFORMATION:
; APPLICANT: Aventis Pharma Deutschland GmbH
; TITLE OF INVENTION: Process for identifying modulators of G protein coupled
; TITLE OF INVENTION: receptors
; FILE REFERENCE: AVE D-2000/A033 englisch
; CURRENT APPLICATION NUMBER: US/11/060,023
; CURRENT FILING DATE: 2005-02-17
; PRIOR APPLICATION NUMBER: US/09/899,295
; PRIOR FILING DATE: 2003-07-06
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 11
; LENGTH: 359
; TYPE: PRT
; ORGANISM: Mus musculus
; US-11-060-023-11

Query Match 46.4%; Score 71; DB 7; Length 359;
Best Local Similarity 48.4%; Pred. No. 0.0048;
Matches 15; Conservative 8; Mismatches 8; Indels 0; Gaps 0;

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DB 16 KEARRINDEIERHVRDKRDARRELKLLLG 46
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US-11-060-023-13
; Sequence 13, Application US/11060023
; Publication No. US20050255531A1
; GENERAL INFORMATION:
; APPLICANT: Aventis Pharma Deutschland GmbH
; TITLE OF INVENTION: Process for identifying modulators of G protein coupled
; TITLE OF INVENTION: receptors
; FILE REFERENCE: AVE D-2000/A033 englisch
; CURRENT APPLICATION NUMBER: US/11/060,023
; CURRENT FILING DATE: 2005-02-17
; PRIOR APPLICATION NUMBER: US/09/899,295
; PRIOR FILING DATE: 2003-07-06
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 13
; LENGTH: 359
; TYPE: PRT
; ORGANISM: Mus musculus
; US-11-060-023-13

Query Match 46.4%; Score 71; DB 7; Length 359;
Best Local Similarity 48.4%; Pred. No. 0.0048;
Matches 15; Conservative 8; Mismatches 8; Indels 0; Gaps 0;

QY 1 KEARKVSRGIDRMLRDQKRDLOQTHRLLLLG 31
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DB 16 KEARRINDEIERHVRDKRDARRELKLLLG 46
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